

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:00:40 ; Search time 29.3505 Seconds
(without alignments)
2351.779 Million cell updates/sec

Title: US-09-446-634A-22
Perfect score: 1804
Sequence: 1 MGIWTLPLVLTSLVARLSS.....KDTSDSENFRNEIQSIV 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	86.0	331	6 Q9TSN4	Q9tsn4 macaca fasc
2	1531	84.9	331	6 Q9BDN0	Q9bdn0 macaca neme
3	1521	84.3	331	6 Q9BDN4	Q9bdn4 cercocobus
4	1509	83.6	333	6 Q9BDP2	Q9bdp2 macaca mula
5	1500	83.1	331	6 Q9GK36	Q9gk36 macaca assa
6	1492.5	82.7	334	6 Q9GL40	Q9gl40 macaca mula
7	1439.5	79.8	310	6 Q9GK28	Q9gk28 macaca arct
8	1377.5	76.4	328	6 Q9BDP0	Q9bdp0 aotus trivi
9	1052.5	58.3	320	6 Q9XSD9	Q9xsd9 oryctolagus
10	1052	58.3	319	6 Q9RV79	Q9rv79 oryctolagus
11	967	53.6	327	6 Q97491	Q97491 oviv aries
12	614.5	34.1	263	6 Q9XS60	Q9xs60 oryctolagus
13	481.5	26.7	150	11 Q9R230	Q9r230 rattus norv
14	478	26.5	147	6 Q8SQ52	Q8sq52 felis silve
15	470	26.1	285	13 Q9DGH7	Q9dgh7 gallus gall
16	463.5	25.7	312	13 Q9DGH8	Q9dgh8 gallus gall

17	429.5	23.8	124	6	Q8SQ51	Q8sq51 felis silve
18	286	15.9	65	6	Q8SQ49	Q8sq49 felis silve
19	246	13.6	357	13	Q9DF34	Q9df34 brachydanio
20	226.5	12.6	368	13	Q57408	Q57408 meleagris g
21	212.5	11.8	438	13	Q9DFV0	Q9dfv0 brachydanio
22	208.5	11.6	387	13	Q9PVD4	Q9pvd4 xenopus lae
23	199	11.0	368	13	Q9IAR7	Q9iar7 gallus gall
24	198	11.0	283	6	Q9XSZ8	Q9xs28 cercopithec
25	189	10.5	368	13	Q9PW79	Q9pw79 gallus gall
26	180	10.0	276	13	Q9DDD2	Q9ddd2 gallus gall
27	179	9.9	401	13	Q9PRG7	Q9prg7 xenopus lae
28	171	9.5	413	11	Q99MM1	Q99mm1 mus musculu
29	170.5	9.5	446	6	Q9SND3	Q9snd3 felis silve
30	168	9.3	186	12	Q9YP87	Q9yp87 cowpox viru
31	163	9.0	186	12	Q9WJB4	Q9wjb4 vaccinia vi
32	161.5	9.0	169	11	Q9JKE0	Q9jke0 rattus norv
33	161.5	9.0	326	12	Q57120	Q57120 cowpox viru
34	161	8.9	186	12	Q72735	Q72735 cowpox viru
35	161	8.9	186	12	Q911R5	Q911r5 vaccinia vi
36	159.5	8.8	350	12	Q57123	Q57123 cowpox viru
37	158.5	8.8	278	6	Q8SQ34	Q8sq34 sus scrofa
38	155.5	8.6	387	11	Q8VD70	Q8vd70 mus musculu
39	153.5	8.5	326	12	Q57122	Q57122 cowpox viru
40	153	8.5	349	12	Q57098	Q57098 camelpox vi
41	153	8.5	349	12	Q8UYA7	Q8uya7 camelpox vi
42	153	8.5	349	12	Q57284	Q57284 camelpox vi
43	152	8.4	347	12	Q57119	Q57119 cowpox viru
44	151.5	8.4	349	12	Q57100	Q57100 monkeypox v
45	151.5	8.4	349	12	Q57102	Q57102 monkeypox v

ALIGNMENTS

RESULT 1

ID	Q9TSN4	PRELIMINARY;	PRT;	331 AA.
AC	Q9TSN4;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	Death receptor Fas (APO-1/CD95).			
GN	FAS.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheidae; Macaca.			
OX	NCBI_TaxID=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20237686; PubMed=10773350;			
RA	Murayama Y., Terao K., Inoue-Murayama M.;			
RT	"Molecular cloning and characterization of cynomolgus monkey Fas.";			
RL	Hum. Immunol. 61:474-485(2000).			
DR	EMBL; AB031420; BAA83551.1; -			
DR	HSSP; P25445; 1DDF.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00531; death; 1.			
DR	Pfam; PF00020; TNFR_c6; 2.			
DR	SMART; SM00005; DEATH; 1.			
DR	SMART; SM00208; TNFR; 2.			
DR	PROSITE; PS00017; DEATH_DOMAIN; 1.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
KW	Receptor.			
SQ	SEQUENCE 331 AA; 37265 MW; OC617508081B05DF CRC64;			

Query Match 86.0%; Score 1552; DB 6; Length 331;
Best Local Similarity 87.2%; Pred. No. 2.2e-121;
Matches 292; Conservative 14; Mismatches 25; Indels 4; Gaps 2;

QY 1 MGIWTLPLVLTSLVARLSSVNAQVTDINSKGLRLKTKVTVTETONLEGLHHDGQFCH 60


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Db      237  AMTLSQVYDFVRKNGVSEAKIDEKNDNVQDTAEQVQLLRNYYQLHGKRDACDTLIKGL 296
QY      299  KKANLCITLAEKIQTIIILKIDTSDSENSFRNEIQSLV 335
Db      297  KTADLCITLAEKIHAVILKIDTSDTENSFGNEVQNLV 333

RESULT 5
Q9GK36 ID Q9GK36 PRELIMINARY; PRT; 331 AA.
AC Q9GK36
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Fas antigen APO-1/CD95.
GN FAS.
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9551;
RN [1]
RP SEQUENCE FROM N.A.
RA Chi L., Shui B., Jiang H., He F.Q., Zhang Y.R., Cai Y.Y.;
RT "Cloning and sequencing of bear monkey Fas antigen cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326208; AAC49382.1;
DR HSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00202; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37167 MW; CE58DB046C67834F CRC64;

Query Match 83.1%; Score 1500; DB 6; Length 331;
Best Local Similarity 84.2%; Pred. No. 4.8e-117;
Matches 282; Conservative 18; Mismatches 31; Indels 4; Gaps

QY 1 MLGTTLLPLVLTSVARLLSSKSNVAQYTDINSGKLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MLGTTLLPLVLTSVARLLSSKSNVAQYTDVSSGKFLRKIVTIEQNLEGLHHEGQPCR 60
QY 61 KPCPPGERKADCTVNGDEPDCVPCQBGKEYTKAHFSSKRCRCRLCDEGHGLEVEINCT 120
Db 61 NPCPPGERKADCTVNEDEPDCVPCQBGKEYTDGHLSSKRCRCRLCDEGHGLEVEINCT 120
QY 121 RTQNTKCRCPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLGWLCLL 180
Db 121 RTQNTKCRCPNFCNSAVCEHCDPCKIKCHGIIIECTLTSTNTKCEEDSRDLPWLCLL 180
QY 181 LLPLPLTWYKRKEVQTKRHKRKNQSGHESPTLPNETVAIINLSDVDLSKYITTTAGVM 240
Db 181 LLLLPPIVYV---VIKACRHKRKNQSGHESPTLPNET-AINLSDVDLSKYITTTAGM 236
QY 241 TLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDKK 296
Db 237 TLSQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQVQPLRNYYQLHGKRDACDTLIKGLKT 296
QY 301 ANLCITLAEKIQTIIILKIDTSDSENSFRNEIQSLV 335
Db 297 ADLCITLAEKIHAVILKIDTSDTENSFGNEVQNLV 331

RESULT 6
Q9GL40 ID Q9GL40 PRELIMINARY; PRT; 334 AA.
AC Q9GL40

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DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Fas antigen.
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Shui B., Chi L., Zhang Y.R.;
RT	"Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY007572; AAG16762.1; ..
DR	HSSP; P25445; 1DDF.
DR	InterPro; IPR000488; Death..
DR	InterPro; IPR001368; TNFR_C6.
DR	Pfam; PF00531; death; 1.
DR	Pfam; PF00020; TNFR_C6; 2.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00208; TNFR; 2.
DR	PROSITE; PS0017; DEATH DOMAIN; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS0050; TNFR_NGFR_2; 2.
SQ	SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;
Query Match 82.7% Score 1492.5; DB 6; Length 334;	
Best Local Similarity 84.0%; Pred. No. 2e-116;	
Matches 284; Conservative 17; Mismatches 30; Indels 7; Gaps	
QY	1 MGIIWTLPLVLTSVARLSKSNVAQVTDINSKGLELRKTVTTVETQNLEGLHHDGFCH 60
Db	1 MLGTWTLLPLVLTSWRLLSKCVIAQTVDISSRGFLRKIVTIEIQNLEGLHHEGQFCR 60
QY	61 KPCPPGERKARDCTVNGDEPDPCVQCQEGEYTKAHFSKKRCRCRLCDDEGHGLEVEINCT 120
Db	61 NPCPPGERKARDCTVNEDEPDPCVQCQEGEYTDKGHFSSKRCRCRLCDDEGHGLEVEINCT 120
QY	121 RTQNTKCRCKPNFFCNFTVCCEHCDPCPKCEHGIIKECTLTSTNKCKEGRSRLGWLC-- 178
Db	121 RTQNTKCRCKPNFFCNFAVCEHCDPCPKCKHGIIECTLTSTNKCKEEDRSRLWLCLL 180
QY	179 -LLLLPTLIIVWKREVKQTKRRKRKENOGSHESPTLNPTVAIINLSDVLSKYITTTA 237
Db	181 LLLLLLPPIVV---VIKKPCRKRKENGGPHESITLNPET-AINLSDVDLSKYITTTA 236
QY	238 GVMTLSOVKGVFKRNGVNEAKIDEIKNDNVQDTAEOKVOLLRNWHOLHGKKEAYDTLIK 297
Db	237 GAMTLSOVKDFGRKNGVSEAKIDEIKNDNVQDTEOKVOLLRNWYQPHGKDCACTDLING 296
QY	298 LKANLCLTAEKTIOTILDKDITSSENSFNRFNIQSIV 335
Db	297 LKTADLCTLAEKHAVILKDKITSNTENSFGNEIQNLV 334
RESULT 7	
Q9GK28	PRELIMINARY; PRT; 310 AA.
ID	Q9GK28;
AC	Q9GK28;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Fas antigen APO-1/CD95.
GN	FAS.
OS	Macaca arctoides (Stump-tailed macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID=9540;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;


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DR PROSITE; PS00652; TNFR_NGFR_1; 1.  
FT PROSITE; PS00652; TNFR_NGFR_2; 2.  
FT VARIANT; 157 159 S -> T.  
SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;  
  
Query Match 76.4%; Score 1377.5; DB 6; Length 328;  
Best Local Similarity 78.7%; Pred. No. 7.6e-107;  
Matches 266; Conservative 21; Mismatches 38; Indels 13; Gaps 5;  
  
QY 1 MGIWTLPLVLTSLVSRSSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 60  
DB 1 MGIWTLPLVLTSLVSRSSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 59  
QY 61 KCPGPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRRCLDEGHGVEINCT 120  
DB 60 KCPGPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRRCLDEGHGVEINCT 119  
QY 121 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIKECTLSNTKCKEESRSNLGW-LCL 179  
DB 120 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIKECTLSNTKCKEESRSNLGW-LCL 179  
QY 180 LLLPIPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSDVDLSKYITTIAGV 239  
DB 180 LLLPIPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSDVDLSKYITTIAGV 239  
QY 240 MTLSQVRFKRVKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTFLKDLK 299  
DB 235 MTLSQVRFKRVKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTFLKDLK 294  
QY 300 KANLCTLAETIQLTILKIDTSSENSNFR--NEIQSLV 335  
DB 295 KANLCTLAETIQLTILKIDTSSENSNFR--NEIQSLV 328  
  
RESULT 9  
Q9XS29 Q9XS29 PRELIMINARY; PRT; 320 AA.  
AC Q9XS29;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE C-type Fas antigen.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isono T., Tanbe Y., Nagano Y., Seto A.;  
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB021299; BAA78431.1; -;  
DR EMBL; AB021296; BAA78428.1; -;  
DR HSP; P25445; IDDF.  
DR InterPro; IPR000488; Death.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR_c6; 3.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00017; DEATH_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.  
DR PROSITE; PS00050; TNFR_NGFR_2; 2.  
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;  
  
Query Match 58.3%; Score 1052.5; DB 6; Length 320;  
Best Local Similarity 61.1%; Pred. No. 9e-80;  
Matches 204; Conservative 36; Mismatches 69; Indels 25; Gaps 5;  
  
QY 1 MGIWTLPLVLTSLVSRSSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 60  
DB 1 MGIWTLPLVLTSLVSRSSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 45  
  
Query Match 58.3%; Score 1052; DB 6; Length 319;  
Best Local Similarity 61.7%; Pred. No. 9.9e-80;  
Matches 206; Conservative 35; Mismatches 67; Indels 26; Gaps 6;  
  
QY 1 MGIWTLPLVLTSLVSRSSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 60  
DB 1 MGIWTLPLVLTSLVSRSSKSVNAQVTDINSKGLERKKTVTETVETONLEGLHHDGQFCH 45  
QY 61 KCPGPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRRCLDEGHGVEINCT 120  
DB 46 QLCPPGTGKKADCTSNEGKPDCEPCQEGEYTDKSHFSKRCRRCLDEGHGVEINCT 105  
QY 121 RTQNTKRCRCPNFCNSTVCEHCDPCTCKEHIKECTLSNTKCKEE---GSRNLGW 176  
DB 106 TIQNTKRCRCPNFCNSTVCEHCDPCTCKEHIKECTLSNTKCKEE---GSRNLGW 165  
QY 177 ICLLLLPLIVVKKREVQKTCRKHKENOGSHESPTLNPTVAINLSDVDLSKYITTI 236  
DB 166 LSTLL-LPIVLGLRR-----YKHKRGKHGDKSTALIPGVPNMFSDVDISKYIPTI 218  
QY 237 AGVMTLSQVRFKRVKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTLIK 296  
DB 1 AGVMTLSQVRFKRVKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTLIK 296
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Db 219 AEEMKINEVFRKNGVNEAKIDIKNDNIQDTAEQKVQLLRNWHQLHKKDAYNTLIK 278
Qy 297 DLKANLCTLAEKIQTIIILKIDTSDSENSERNE 330
   :||||| :||||| :||||| :| :| :|
Db 279 GLRKNALCALAEKIQDIYQKIDTSDHNDLIRDE 312

RESULT 11
O97491 .
ID O97491 PRELIMINARY; PRT; 327 AA.
AC O97491;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fas protein.
GN FAS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOCTE;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT "Cloning of sheep fas antigen."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1;
DR HSP; P25445; IODF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00031; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;

Query Match 53.6%; Score 967; DB 6; Length 327;
Best Local Similarity 56.7%; Pred. No. 1.2e-72;
Matches 190; Conservative 47; Mismatches 90; Indels 8; Gaps 3;

Qy 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVETQNLGLHHDGQFCH 60
Db 1 MSGIWHLSLIFTSVSRPLSKGENAHVAGINSEGLRKNITGASSCQ-EGLYREHLFC 59
Qy 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDGEGHGLEVEINCT 120
Db 60 QCPGGRKRGDCRKGDDMPCEVLCSEGEYTDKSHHDKCIRCSVCDEEHGLEVEHNCT 119
Qy 121 RTQNTKRCRKNPFNCSTVCEHCDPCTKCEHGIKCTLTSTNTKKEGSRSLNGLWLL 180
Db 120 RTQNTKRCRCKSNFNCSTVCEHCDPCTKCEHGIKCTLTSTNTKKGSRSHNSLWALLI 179
Qy 181 LLPILVWVKRKEVQKTKRKHKNQSGHESPTLNPETVAINLSVDLSKYITTIAGVM 240
Db 180 LLLLLIFLIYKVVW-RRRNKKNKNCVSAASDEGRQLNLTVDLGLKYPSTAEML 236
Qy 241 TLISOVGEVFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHKKDAYNTLIK 240
Db 237 KTEVEFRKNGVNEAKIDDIHNDLHETAEQKVQLLRKWKYQSHGKNAYCTLTAKLPK 296
Qy 301 ANLCTLAEKIQTIIILKIDTSDSENSERNEIQSLV 335
Db 297 A----LAEKICIVLKDIINERANLQNESNLV 327

RESULT 12
Q9XS60
ID Q9XS60 PRELIMINARY; PRT; 263 AA.
AC Q9XS60;
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DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fas antigen spliced variant.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RT Isono T., Tanbe Y., Nagano Y., Seto A.;
RA "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021297; BAA78429.1;
DR HSP; P25445; IODF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 263 AA; 30374 MW; 6D76782ADED1BED7 CRC64;

Query Match 34.1%; Score 614.5; DB 6; Length 263;
Best Local Similarity 53.8%; Pred. No. 2.3e-43;
Matches 119; Conservative 23; Mismatches 54; Indels 25; Gaps 5;

Qy 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVETQNLGLHHDGQFCH 60
Db 1 MTGIWLLPLILACIAGSLSTIN----DCKIKN-----ETQYSTG-YLSGNFCC 45
Qy 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDGEGHGLEVEINCT 120
Db 46 QLCPGPGTKKADCTSNKGRPDCEPCEGEYTDKSHFSKRCRCRLCDGEGHGLEVEINCT 105
Qy 121 RTQNTKRCRKNPFNCSTVCEHCDPCTKCEHGIKCTLTSTNTKKEE---GSRSLGW 176
Db 106 TIQNTKRCRCKSNFNCALKEHCDPCTKCEHGIKCTLTSTNTKKEE---GSRSLGW 165
Qy 177 LCLLLPIPLVWVKRKEVQKTKRKHKNQSGHESPTLNP 217
Db 166 LCLLLPIPLVGLRR-----YKHRDGHGDKSTALIP 200

RESULT 13
Q9R230
ID Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-CORPUS LUTEUM;
RA Lareu R.R., Dharmarajan A.;
RT "Cloning and expression of Fas and Fas Ligand in the apoptotic rat corpus luteum."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD20221.1;
DR HSP; P25942; IODF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON_TER 150
FT NON_TER 150
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;
```

```
Query Match 26.7%; Score 481.5; DB 11; Length 150;
Best Local Similarity 55.6%; Pred. No. 1.4e-32;
Matches 85; Conservative 21; Mismatches 42; Indels 5; Gaps 2;

QY 7 LLPVLTSVARLSKSNVAQVTDINSGLRLKRTVTVTYTONLEGLHHDGQFCHKPCPPG 66
Db 2 VPLVLVLAG---PELVNMQGTDSISGLLEKRSVRETDNNCSGLYQVGFPCQCPQGP 57
QY 67 ERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLCDEGHGLEVEINLCTRTONTK 126
Db 58 ERKVKDCTTSGGAPCTHPCYEGEYTDKRYSDKRCACFCDEGHGLEVEINLCTRTONTK 117
QY 127 CRCKPNFFCSTVCEHCDPCTKCE-HGIIKECT 158
Db 118 CRCKENFYCNALCDHCYHCTSCGLEIDLEPCT 150

RESULT 14
Q8SQ52 PRELIMINARY; PRT; 147 AA.
AC Q8SQ52;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Fas (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AB072009; BAB86798.1;
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 26.5%; Score 478; DB 6; Length 147;
Best Local Similarity 55.1%; Pred. No. 2.7e-32;
Matches 86; Conservative 24; Mismatches 32; Indels 14; Gaps 3;

QY 86 QEGKEYTDKAHFSSKRCRCLCDEGHGLEVEINLCTRTONTKCRCKPNFFCSTVCEHCDP 145
Db 1 EEAADYDRSHFSPRCRCKICDEEHGLEVEKNCRTONTKCRCKSNFFCNVQCQDHCNP 60
QY 146 CTKEHGIIKECTLTSNTCKEGRSRLNGLWCLLLPIPLIYVWKRKEVQKTC---RK 201
Db 61 CMWCEHGILENCTPTNTCK-KQSSSKLLWLCALLILPSAL-----VCCCVLKK 110
QY 202 HRKENGSHSPTLNPETVAINLSDVLSKYITIA 237
Db 111 YRNTKNGRRRESTVITESMPNFTDIDLKYISSIA 146

RESULT 15
Q9DGH7 PRELIMINARY; PRT; 285 AA.
AC Q9DGH7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Fas ligand receptor soluble form (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RA Bridgham J.T., Johnson A.L.;
RT "Fas Expression and Regulation in Hen Granulosa Cells."
RL Submitted (JUG-2000) to the EMBL/GenBank/DBJ databases:
DR EMBL; AP296675; AGO2243.1;
DR HSSP; O14763; ID4V.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00405; DEATH; 1.
DR SMART; SM00408; TNFR; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 285 AA; 32431 MW; A9761960CCD79B6D CRC64;

Query Match 26.1%; Score 470; DB 13; Length 285;
Best Local Similarity 37.7%; Pred. No. 2.8e-31;
Matches 104; Conservative 43; Mismatches 101; Indels 28; Gaps 5;

QY 56 GQFCHKFCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLCDEGHGLEV 115
Db 4 GQCCTK-CRGRHVKSIDCPKT--OEHCVPCKGEEYMDHINDLDECMRCSRCDKALGLEV 60
QY 116 EINCTRTONTKCRCKPNFFCSTVCEHCDPCTKCEHG-IIKECTLTSNTCKEGRSRLN 174
Db 61 VKNCTSTENAECSAKNHYCNSSRCEHCESTVCNGQIEKECTSTSTVCRMQ----- 114
QY 175 GWLCLLLPIPLIYVWKRKEVQKTCRKHRENQGSHPSTLNPETVAINLSDVLSKYIT 234
Db 115 -----VKRKVNNTTQGN---TAAADTKGVHSPETLRLIHIDVLTTHVP 156
QY 235 TIAGVWLSQVKGVKNGVNEAKIDEIKNDNVODTAEQKVLRLNHLHGKKEAYDTL 294
Db 157 DIVREMTLEQVMTFVRHRLSEPTIEETLLDLSNNTSEQIKLQKQWYQKHGMGGAYETL 216
QY 295 IKDLKANLCTLAEKIOTIILKIDITSDSSENSFNENE 330
Db 217 ICSRLDKMRTAADKIERKKAAYCSHQRRESYND 252

Search completed: May 9, 2003, 17:06:47
Job time : 32.3505 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:57:39 ; Search time 54.3354 Seconds
(without alignments)
801.926 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIAVPLVLVLAGSOLVRH.....KDLGKSTPTDGTENEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	14	AA1980.DAT.* Murine Fas. Mus m
2	1804	100.0	327	16	AA1981.DAT.* Murine Fas. antigen
3	1804	100.0	327	17	AA1982.DAT.* mfas sequence. Sy
4	1804	100.0	327	21	AA1934.DAT.* Amino acid sequenc
5	1800	99.8	327	20	AA1934.DAT.* Fas ligand (FasL)
6	1001	55.5	576	16	AA1986.DAT.* Expression vector
7	981	54.4	592	17	AA1987.DAT.* Fas antigen #2. S
8	977	54.2	169	16	AA1986.DAT.* Plasmid fragment p
9	863.5	47.9	669	19	AA1986.DAT.* Human TNFRI protei
10	856	47.5	335	13	AA1980.DAT.* Human cell surface

11	856	47.5	335	16	AA1980.DAT.* Human Fas protein.
12	856	47.5	335	17	AA1981.DAT.* Human Fas antigen.
13	856	47.5	335	17	AA1982.DAT.* hfas from plasmid
14	856	47.5	335	18	AA1983.DAT.* Human Fas antigen.
15	856	47.5	335	19	AA1984.DAT.* Fas protein. Mamm
16	856	47.5	335	21	AA1934.DAT.* Amino acid encodin
17	856	47.5	335	21	AA1934.DAT.* CD-95 (FAS/APO-1)
18	856	47.5	335	22	AA1935.DAT.* Human tumour necro
19	844	46.8	335	21	AA1935.DAT.* Human Fas receptor
20	825	45.7	331	22	AA1935.DAT.* Human Fas receptor
21	810.5	44.9	314	16	AA1935.DAT.* Fas-delta-TM. Hom
22	810.5	44.9	314	17	AA1935.DAT.* Human Fas soluble
23	801.5	44.4	314	20	AA1935.DAT.* Soluble Fas recept
24	676.5	37.5	170	21	AA1935.DAT.* Rat Fas receptor.
25	645	35.8	281	21	AA1935.DAT.* Human Fas. Homo s
26	585	32.4	219	22	AA1935.DAT.* Fas protein. Unid
27	530	29.4	173	21	AA1935.DAT.* Human Fas receptor
28	530	29.4	600	16	AA1935.DAT.* Expression vector
29	523	29.0	237	21	AA1935.DAT.* Human colon cancer
30	520	28.8	600	17	AA1935.DAT.* Fas antigen #1. S
31	494.5	27.4	144	18	AA1935.DAT.* Human Fas antigen
32	494.5	27.4	159	18	AA1935.DAT.* Human Fas antigen
33	494.5	27.4	376	18	AA1935.DAT.* Human Fas antigen
34	494.5	27.4	376	19	AA1935.DAT.* Antigenic peptide
35	482	26.7	86	23	AA1935.DAT.* Nucleic acid seale
36	341	18.9	431	22	AA1935.DAT.* CD44HextraFasTm/cy
37	340.5	18.9	920	22	AA1935.DAT.* Flt-1HextraFasTm/cy
38	339	18.8	927	22	AA1935.DAT.* Flk-1HextraFasTm/cy
39	332	18.4	436	21	AA1935.DAT.* Apoptobody3sc fusl
40	319.5	17.7	436	22	AA1935.DAT.* CD44HextraFasTm/cy
41	305.5	16.9	149	17	AA1935.DAT.* Human Fas soluble
42	281	15.6	121	23	AA1935.DAT.* Tumour necrosis fa
43	278.5	15.4	111	23	AA1935.DAT.* Tumour necrosis fa
44	226	12.5	84	22	AA1935.DAT.* Fas/Apo-1/CD95 Dea
45	220	12.2	84	19	AA1935.DAT.* Fas-R protein frag

ALIGNMENTS

RESULT 1
AAR41688
ID AAR41688 standard; Protein: 327 AA.
XX AAR41688;
AC AAR41688;
XX 19-APR-1994 (first entry)
XX Murine Fas.
XX Murine Fas;
XX Murine; Fas; human; macrophage; cell strain; BAM3.
XX Mus musculus.
XX JP05219959-A.
XX 31-AUG-1993.
XX 14-FEB-1992; 92JP-0028090.
XX 14-FEB-1992; 92JP-0028090.
XX (OSAB-) 2H OSAKA BIOSCIENCE KENKYUSHO.
XX WPI; 1993-308326/39.
XX N-PSDB; AAQ48008.
XX DNA hybridising with sequence coding for human Fas protein - is
XX prepd. from e.g. BAM3 cell of mouse macrophage cell
XX Claim 1; Page 6-7; 8pp; Japanese.
XX This sequence represents the murine Fas protein. The cDNA encoding

CC this sequence hybridises with the human Fas gene and was isolated
CC from the mouse macrophage cell strain BAM3. This sequence may be
CC used for the production of large amounts of murine Fas.

XX Sequence 327 AA;

Query Match 100.0%; Score 1804; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.1e-140;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCQPCQ 60
DB 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCQPCQ 60
QY 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
DB 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
QY 121 TKCKCKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
DB 121 TKCKCKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
QY 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
DB 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
QY 241 ARENNIKEGKIDETIMHDSIQDTAEQVQLLLCWYQSHGKSDAYQDLIKGLKKAECRTILD 300
DB 241 ARENNIKEGKIDETIMHDSIQDTAEQVQLLLCWYQSHGKSDAYQDLIKGLKKAECRTILD 300
QY 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
DB 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327

RESULT 2

AAR78611
ID AAR78611 standard; Protein; 327 AA.

XX AAR78611;

XX 19-FEB-1996 (first entry)

XX Murine Fas antigen extracellular region.

XX Murine Fas antigen; extracellular region; soluble membrane protein;
KW antibody production; diseases; treatment; prevention.

XX Mus musculus.

XX Key Location/Qualifiers
FH Peptide 1..21
FT Peptide /label= sig_peptide
FT Peptide 22..327
FT Peptide /label= mat_peptide

XX JP07115988-A.

XX 09-MAY-1995.

XX 26-OCT-1993; 93JP-0267644.

XX 26-OCT-1993; 93JP-0267644.

XX (NIBS) JAPAN TOBACCO INC.

XX WPI; 1995-202847/27.

XX N-PSDB; AAQ95302.

XX Preparation of soluble membrane proteins - for their use in antibody
PT production for the treatment and prevention of related diseases

XX Example 2; Pages 32-33; 51pp; Japanese.

XX

CC AAQ95302 encodes AAR78611 the murine Fas antigen extracellular region.
CC The cDNA was used in the construction of an expression vector for
CC the prodn. of recombinant soluble membrane proteins. The proteins
CC can be used in antibody prodn. for the treatment and prevention of
CC related diseases.

XX Sequence 327 AA;

Query Match 100.0%; Score 1804; DB 16; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.1e-140;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCQPCQ 60
DB 1 MLWIAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPFCQPCQ 60
QY 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
DB 61 PGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCCTLCDEEHGLEVEVETNCTLTQN 120
QY 121 TKCKCKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
DB 121 TKCKCKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPNRNLWLLTILVLLI 180
QY 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
DB 181 PLVFIYRKRYKRCWKRRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
QY 241 ARENNIKEGKIDETIMHDSIQDTAEQVQLLLCWYQSHGKSDAYQDLIKGLKKAECRTILD 300
DB 241 ARENNIKEGKIDETIMHDSIQDTAEQVQLLLCWYQSHGKSDAYQDLIKGLKKAECRTILD 300
QY 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
DB 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327

RESULT 3

AAR92530

ID AAR92530 standard; Protein; 327 AA.

XX AAR92530;

XX 06-SEP-1996 (first entry)

XX mFas sequence.

XX

KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.

XX Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..21
FT Peptide /note= "signal peptide"
FT Protein 22..327
FT Protein /note= "mature Fas"
FT Misc-difference 24
FT /note= "encoded by AGT"

XX WO9601277-A1.

XX 18-JAN-1996.

XX 03-MAR-1995; 95WO-JP00349.

XX 14-FEB-1995; 95JP-0025637.

XX 06-JUL-1994; 94JP-0154706.

XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

XX (NIBS) JAPAN TOBACCO INC.

XX

PI Hachiya T, Noguchi J, Yonehara S;
 XX WPI: 1996-087635/09.
 DR N-PSDB; AAT16305.
 XX
 XX Immunoassay method for soluble Fas antigen in body fluids - for
 PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
 PT systemic lupus erythematosus
 XX
 XX Example 9; Page 80-82; 124pp; Japanese.
 PS
 XX This sequence represents the mFas antigen used for the mFas.EXT,
 CC contained within the plasmid pME18S. The soluble Fas antigen is included
 CC in the immunoassay kit for the invention. The kit is for the assay of
 CC soluble Fas antigen and contains an immobilised anti-soluble Fas
 CC monoclonal antibody, as well as the standard soluble Fas antigen
 CC represented by this sequence. The assay is simple and has high accuracy,
 CC high sensitivity, and is capable of assaying a number of different
 CC specimens at the same time. The immunoassay is used on biological
 CC samples (such as serum) and is useful for diagnosis of autoimmune
 CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
 CC (SLE).
 XX
 SQ Sequence 327 AA;
 Query Match 100.0%; Score 1804; DB 17; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.1e-140;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 DB 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 QY 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 DB 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 QY 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTLVLLI 180
 DB 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTLVLLI 180
 QY 181 PLVFIYKRYKRRKCKWRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
 DB 181 PLVFIYKRYKRRKCKWRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
 QY 241 ARENNIEGKIDEIMHDSIQDTAEQVOLLICWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 DB 241 ARENNIEGKIDEIMHDSIQDTAEQVOLLICWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 QY 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 DB 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 RESULT 4
 AAB19344
 ID AAB19344 standard; Protein: 327 AA.
 XX
 AC AAB19344;
 XX
 XX 06-MAR-2001 (first entry)
 DT
 XX Amino acid sequence of a murine Fas (Apo-1) protein.
 DE
 XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
 KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
 KW autoimmune disease; inflammatory disease; lymphoma.
 XX
 OS Mus musculus.
 XX
 XX W0200061150-A1.
 PN
 XX 19-OCT-2000.
 PD

XX 10-APR-2000; 2000WO-US09540.
 PF
 XX 12-APR-1999; 99US-0290640.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Dean NM, Marcussen EG;
 PI
 XX WPI: 2000-628395/60.
 DR
 DR N-PSDB; AAC1859.
 XX
 PT Antisense oligonucleotides for treating hepatitis and colon, liver or
 PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
 PT 1 (Fap-1) expression
 XX
 XX Example 5; Page 108-109; 116pp; English.
 PS
 XX The present sequence represents murine Fas (Apo-1). The specification
 CC describes antisense compounds which are targeted to the 5'-untranslated
 CC region, translational start site, translational termination region
 CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
 CC ligand (FasL), or Fap-1 (Fas associated protein.1, protein tyrosine
 CC phosphatase). The antisense compounds are used to inhibit the
 CC expression of Fas, FasL or Fap-1 in cells or tissues. They are used
 CC to treat autoimmune or inflammatory diseases such as hepatitis. They
 CC can also be used to treat cancer, especially colon, liver or lung
 CC cancer or lymphoma.
 XX
 SQ Sequence 327 AA;
 Query Match 100.0%; Score 1804; DB 21; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.1e-140;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 DB 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQPCQ 60
 QY 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 DB 61 PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVETNCTLTQN 120
 QY 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTLVLLI 180
 DB 121 TKCKCKPDFYCDSPGCEHCVRASCSEHGTLEPCTATNTNCRKQSPRNLWLLTLVLLI 180
 QY 181 PLVFIYKRYKRRKCKWRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
 DB 181 PLVFIYKRYKRRKCKWRQDDPESRTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
 QY 241 ARENNIEGKIDEIMHDSIQDTAEQVOLLICWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 DB 241 ARENNIEGKIDEIMHDSIQDTAEQVOLLICWYQSHGKSDAYQDLIKGLAKACRRRLD 300
 QY 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 DB 301 KFDQMVQKDLGKSTPDTGNEGQCLE 327
 RESULT 5
 AAW86241
 ID AAW86241 standard; Protein: 327 AA.
 XX
 AC AAW86241;
 XX
 XX 16-FEB-1999 (first entry)
 DT
 XX Fas ligand (FasL) protein.
 XX
 XX Fas ligand; FasL; Fas receptor; tumour; non-tumourigenic; T cell;
 KW rhabdomyosarcoma; killing; myoblast cell; immune provocation;
 KW neutrophil; detection.

```

XX OS Mus sp.
XX
XX PN W09846242-A1.
XX
XX PD 22-OCT-1998.
XX
XX PF 10-APR-1998; 98WO-US07235.
XX
XX PR 11-APR-1997; 97US-0041880.
XX
XX PA (STRD ) UNIV STANFORD.
XX
XX PI Blau HM, Hofmann A;
XX
XX DR WPI; 1999-009332/01.
XX
XX DR N-PSDB; AAV71961.
XX
XX
XX PT Killing tumour cells which express the Fas receptor - by
XX PT administering non-tumourigenic cells that express the Fas ligand to
XX PT kill the tumour cells, e.g. rhabdomyosarcoma cells
XX
XX PS Examples; Pages 23-25; 42pp; English.
XX
XX CC This represents a Fas ligand (FasL) protein. This can be used in the
XX CC method of the invention of killing of tumour cells which express the
XX CC Fas receptor. The method comprises administering non-tumourigenic cells
XX CC that express the FasL to kill the tumour cells. Rhabdomyosarcoma cells
XX CC which express the Fas receptor can also be killed by administering
XX CC myoblast cells that express the FasL. The methods can be used for the
XX CC destruction of Fas receptor expressing tumour cells. They also provide a
XX CC general immune provocation that stimulates the clearance of the tumour
XX CC cells involving the infiltration of neutrophils into the area of
XX CC administration of Fas-expressing cells and also the infiltration of
XX CC T cells. The methods can also be used for the detection of the Fas
XX CC receptor on cells.
XX
XX SQ Sequence 327 AA;
XX
XX Query Match 99.8%; Score 1800; DB 20; Length 327;
XX Best Local Similarity 99.7%; Pred. No. 8.8e-140;
XX Matches 326; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLWIWAVPLVLAGSQLRVHTQGTNSISLSKLRRRVHETDKNCSEGLYGGPFCPCQ 60
XX |||||
XX Db 1 MLWIWAVPLVLAGSQLRVHTQGTNSISLSKLRRRVHETDKNCSEGLYGGPFCPCQ 60
XX |||||
XX QY 61 PGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
XX |||||
XX Db 61 PGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
XX |||||
XX QY 121 TKCKCKPDEFYCDSPGCEHCVCASCSEHGTLPECTATNTNCRKQSPNRRLWLLTILVLLI 180
XX |||||
XX Db 121 TKCKCKPDEFYCDSPGCEHCVCASCSEHGTLPECTATNTNCRKQSPNRRLWLLTILVLLI 180
XX |||||
XX QY 181 PLVFIYKRYKRCWKRRDDPSRTSSRETIPMNASNLSLSKYIPRIAEQAKKF 240
XX |||||
XX Db 181 PLVFIYKRYKRCWKRRDDPSRTSSRETIPMNASNLSLSKYIPRIAEQAKKF 240
XX |||||
XX QY 241 ARNNKEGKIDIMHDSIQTAEQVQLLQWYQSHGSKSDAYQDLIKLKAECRRRLD 300
XX |||||
XX Db 241 ARNNKEGKIDIMHDSIQTAEQVQLLQWYQSHGSKSDAYQDLIKLKAECRRRLD 300
XX |||||
XX QY 301 KFDQMWQKDLGKSTPDTGNENEGQCLE 327
XX |||||
XX Db 301 KFDQMWQKDLGKSTPDTGNENEGQCLE 327
XX |||||
XX
XX RESULT 6
XX AAR78613
XX ID AAR78613 standard; Protein; 576 AA.
XX
XX OS AAR78613;

```

```

XX XX 20-FEB-1996 (first entry)
XX XX Expression vector pME18S/mFas.EXT-AIC2A protein prod.
XX XX
XX DE Expression vector; pME18S/mFas.EXT-AIC2A; murine Fas antigen;
XX KW extracellular; region; AIC2A; soluble membrane protein;
XX KW antibody production; diseases; treatment; prevention.
XX
XX OS Mus musculus.
XX
XX PN JP07115988-A.
XX
XX PD 09-MAY-1995.
XX
XX PF 26-OCT-1993; 93JP-0267644.
XX
XX PR 26-OCT-1993; 93JP-0267644.
XX
XX PA (NIBS ) JAPAN TOBACCO INC.
XX
XX DR WPI; 1995-202847/27.
XX DR N-PSDB; AAQ95306.
XX
XX PT Preparation of soluble membrane proteins - for their use in antibody
XX PT production for the treatment and prevention of related diseases
XX
XX PS Claim 10; Pages 36-38; 51pp; Japanese.
XX
XX CC AAR78613 is the protein prod. of the expression vector pME18S/murine Fas
XX CC antigen-extracellular region-AIC2A. The expression vector was used for
XX CC the prodn. of recombinant soluble membrane proteins. The proteins can
XX CC be used in antibody prodn. for the treatment and prevention of related
XX CC diseases.
XX
XX SQ Sequence 576 AA;
XX
XX Query Match 55.5%; Score 1001; DB 16; Length 576;
XX Best Local Similarity 91.2%; Pred. No. 8e-74;
XX Matches 177; Conservative 3; Mismatches 12; Indels 2; Gaps 1;
XX
XX QY 1 MLWIWAVPLVLAGSQLRVHTQGTNSISLSKLRRRVHETDKNCSEGLYGGPFCPCQ 60
XX |||||
XX Db 1 MLWIWAVPLVLAGSQLRVHTQGTNSISLSKLRRRVHETDKNCSEGLYGGPFCPCQ 60
XX |||||
XX QY 61 PGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
XX |||||
XX Db 61 PGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
XX |||||
XX QY 121 TKCKCKPDEFYCDSPGCEHCVCASCSEHGTLPECTATNTNCRKQSPNRRLWLLTILVLLI 180
XX |||||
XX Db 121 TKCKCKPDEFYCDSPGCEHCVCASCSEHGTLPECTATNTNCRKQSPNRRLWLLTILVLLI 180
XX |||||
XX QY 181 PLVFI--YRKRYKR 192
XX || : | : |
XX Db 181 PLKTLICYNDYTNR 194
XX
XX RESULT 7
XX AAR92527
XX ID AAR92527 standard; Protein; 592 AA.
XX
XX AC AAR92527;
XX
XX DT 06-SEP-1996 (first entry)
XX
XX DE Fas antigen #2.
XX
XX KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
XX KW rheumatoid arthritis; serum; systemic lupus erythematosus.
XX
XX OS Synthetic.
XX

```


FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT 22..592
FT /note= "mature Fas antigen #2"

XX WO9601277-A1.
XX 18-JAN-1996.
XX 03-MAR-1995; 95WO-JP00349.
XX 14-FEB-1995; 95JP-0025637.
XX 06-JUL-1994; 94JP-0154706.
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX (NIBS) JAPAN TOBACCO INC.

XX Hachiya T, Noguchi J, Yonehara S;
XX WPI: 1996-087635/09.
XX N-PSDB; AAR16301.

XX Immunoassay method for soluble Fas antigen in body fluids - for
PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
PT systemic lupus erythematosus

XX Claim 11; Page 87-91; 124pp; Japanese.

XX AAR9526 and AAR9527 represent soluble Fas antigens. These soluble Fas
CC antigen is included in the immunoassay kit of the invention. The kit is
CC for the assay of soluble Fas antigen and contains an immobilised
CC anti-soluble Fas monoclonal antibody, as well as one of these standard
CC soluble Fas antigens. The assay is simple and has high accuracy, high
CC sensitivity, and is capable of assaying a number of different specimens
CC at the same time. The immunoassay is used on biological samples (such
CC as serum) and is useful for diagnosis of autoimmune diseases such as
CC rheumatoid arthritis or systemic lupus erythematosus (SLE).

XX Sequence 592 AA;

Query Match 54.4%; Score 981; DB 17; Length 592;
Best Local Similarity 89.2%; Pred. No. 3.7e-72;
Matches 173; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYGGPCCPCQ 60
DB 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYGGPCCPCQ 60

QY 61 PGRKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN 120
DB 61 PGRKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN 120

QY 121 TKCKCKPDFYCDSPGCEHVCASCSEHGTLEPCTATNTNCRKOSPRNRLWLLTILVLLI 180
DB 121 TKCKCKPDFYCDSPGCEHVCASCSEHGTLEPCTATNTNCRKOSPRNRLWLLTILVLLI 180

QY 181 PLVFI--YRKYRK 192
DB 181 PLKTECINDYTNR 194

RESULT 8
AAR78612
ID AAR78612 standard; Protein: 169 AA.

XX AAR78612;

XX 19-FEB-1996 (first entry)

XX Plasmid fragment pME18s expression prod.

XX Plasmid pME18s; soluble membrane protein; fragment;

KW antibody production; diseases; treatment; prevention.

XX Synthetic.

XX Key Location/Qualifiers
FT Peptide 1..21
FT /label= sig_peptide
FT 22..169
FT /label= mat_peptide

XX JP07115988-A;
XX 09-MAY-1995.
XX 26-OCT-1993; 93JP-0267644.
XX 26-OCT-1993; 93JP-0267644.
XX (NIBS) JAPAN TOBACCO INC.
XX WPI: 1995-202847/27.
XX N-PSDB; AAQ55305.

XX Preparation of soluble membrane proteins - for their use in antibody
PT production for the treatment and prevention of related diseases
XX Example 2; Pages 34-35; 51pp; Japanese.

XX AAQ5305 is the plasmid fragment pME18s which encodes AAR78612. The
CC plasmid was used in the construction of an expression vector for
CC the prodn. of recombinant soluble membrane proteins. The proteins
CC can be used in antibody prodn. for the treatment and prevention of
CC related diseases.

XX Sequence 169 AA;

Query Match 54.2%; Score 977; DB 16; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.7e-72;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYGGPCCPCQ 60
DB 1 MLWTWAVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYGGPCCPCQ 60

QY 61 PGRKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN 120
DB 61 PGRKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVETNCTLTQN 120

QY 121 TKCKCKPDFYCDSPGCEHVCASCSEHGTLEPCTATNTNCRKOSPRNR 169
DB 121 TKCKCKPDFYCDSPGCEHVCASCSEHGTLEPCTATNTNCRKOSPRNR 169

RESULT 9
AAW64484
ID AAW64484 standard; Protein: 669 AA.

XX AAW64484;

XX 20-OCT-1998 (first entry)

XX Human TNFR1 protein.

XX Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;
KW agonist; tumour necrosis factor; TNF; ligand; autoimmune disease;
KW infection; graft rejection; antagonist; inhibitor; diagnostic.

XX Homo sapiens.

XX WO9832856-A1.

XX 30-JUL-1998.


```
QY 233 TIOAKKFARENNIKEGIDEIMHDSIQDTAEQKVOLLWCYQSHGSKSDAYODLIKGLKK 292
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 241 TISOVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 293 AECRTLDKFQDMVKDGLGKSTPDTGNEGQCL 326
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 301 ANLCTLAETKIQTIIILKDTSDSENSFRNETQSL 334
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
AAR78606
ID AAR78606 standard; Protein; 335 AA.
XX
AC AAR78606;
XX
DT 19-FEB-1996 (first entry)
XX
DE Human Fas protein.
XX
KW Plasmid pF58; human Fas cDNA; soluble membrane protein;
XX antibody production; diseases; treatment; prevention.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT /label= sig_peptide
FT Peptide 17..335
FT /label= mat_peptide
FT
XX JP07115988-A.
XX
XX 09-MAY-1995.
XX
XX 26-OCT-1993; 93JP-0267644.
XX
XX 26-OCT-1993; 93JP-0267644.
XX
XX (NLSB ) JAPAN TOBACCO INC.
XX
XX WPI; 1995-202847/27.
XX N-PSDB; AAQ95297.
XX
XX Preparation of soluble membrane proteins - for their use in antibody
XX production for the treatment and prevention of related diseases
XX
XX Example 1; Pages 15-17; 51pp; Japanese.
XX
XX AAR78606 (human Fas protein) is encoded by the plasmid pF58 which
XX contains hFas cDNA. The plasmid was used in the construction of an
XX expression vector for the prodn. of recombinant soluble membrane
XX proteins. The proteins can be used in antibody prodn. for the
XX treatment and prevention of related diseases.
XX
XX Sequence 335 AA;
XX
Query Match 47.58; Score 856; DB 16; Length 335;
Best Local Similarity 49.4%; Pred. No. 3.4e-62;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWTWAVLPLVLG-----SQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYOGGPCC 56
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MGLTWLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVTQNLEGLHHDGQFCH 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 57 QPCPGKRVKVEDCKRMGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEETNCT 116
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEVTDRAHFSSKRCRCLCDEGHGLEVEINCT 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 LTQNTKCKKPDFCDSPGCHVCRCASCEHGTLEPCTATNTNCRKPSRNLMLLIL 176
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 RTQNTKRCCKNFNFCNSTVCECHDPCFTKCEHGIIECTLTNTKCKEGRSLNGLWCLL 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 VLLIPL-VFIYRKYRKRKCRWRQDDP---ESRTSSRETIPMNASNLSLSKYIPRIADM 232
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
DB 181 LLIPLIIVVRRKEVQKTCRHRKENGQSHESPTLNPTETVAIINLSDVLSKYITTIAGVM 240
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 233 TIOAKKFARENNIKEGIDEIMHDSIQDTAEQKVOLLWCYQSHGSKSDAYODLIKGLKK 292
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 241 TISOVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 293 AECRTLDKFQDMVKDGLGKSTPDTGNEGQCL 326
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 301 ANLCTLAETKIQTIIILKDTSDSENSFRNETQSL 334
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 12
AAR99681
ID AAR99681 standard; Protein; 335 AA.
XX
AC AAR99681;
XX
DT 10-OCT-1996 (first entry)
XX
DE Human Fas antigen.
XX
KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
XX angioimmunoblastic lymphadenopathy; AILD.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT /label= Sig_peptide
FT Protein 17..335
FT /label= Mat_protein
FT Domain 17..173
FT /label= Extracellular_domain
FT Domain 174..190
FT /label= Transmembrane_domain
FT Domain 191..335
FT /label= Cytoplasmic_tail
XX
XX WO9620206-A1.
XX
XX 04-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17083.
XX
XX 23-DEC-1994; 94US-0371263.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Cheng J, Liu C, Mountz JD, Zhou T;
XX
XX WPI; 1996-321796/32.
XX N-PSDB; AAT34526.
XX
XX Natural, soluble form of Fas antigen secreted by human cells is
XX result of alternative mRNA processing - used to diagnose
XX Fas-associated disease, e.g. systemic lupus erythematosus
XX
XX Disclosure; Page 109-111; 152pp; English.
XX
XX A cDNA clone (AAT34526) codes for a membrane receptor-like protein,
XX Fas antigen (AAR99681). It was isolated from cDNA derived from the
XX peripheral blood mononuclear cells of systemic lupus erythematosus
XX (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients. 4
XX Soluble variants (AAR99682-85) were identified of the Fas antigen.
XX These arose by alternative splicing of Fas gene transcripts. The
XX Fas variants were present at higher levels in SLE and AILD patients
XX than the non-soluble Fas antigen.
XX
XX Sequence 335 AA;
XX
Query Match 47.5%; Score 856; DB 17; Length 335;
Best Local Similarity 49.4%; Pred. No. 3.4e-62;
```

Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

```

QY 1 MLWIAVLPLVLG-----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGGPFC 56
DB 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKTVTVTQNLGLHHDGQFCH 60
QY 57 QPCQPGKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCLCDEEHGLEVEYNCT 116
DB 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGLEVEINCT 120
QY 117 LTQNTKCKKDPDYCDSPGCEHCVRCAECHEGTLPCTATSNCRKQSPRNLMLLTL 176
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTKCKEGRSNLGLCLL 180
QY 177 VLLIPL-VFIYRKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLKSVIPIRIADM 232
DB 181 LLPIPLIIVWKRKEVQKCRKRKENQGSHPSTLPETVAINLSVDVLSKYIITIAQVM 240
QY 233 TIQEAKEFARENNIKEGIDIMHDSIODTAQKQVOLLCHWYQSHGKSDAYQDLIKGLK 292
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLK 300
QY 293 AECRRTLDKQDMQKDLGKSTPDTGNEGQCL 326
DB 301 ANLCTLAETIQTILKADITSDSENSFRNEIQSL 334

```

RESULT 13
AAW50289

ID AAW50289 standard; Protein; 335 AA.

AC AAW50289;

DT 06-SEP-1996 (first entry)

XX hFas from plasmid pCEV4/hFas.

Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
rheumatoid arthritis; serum; systemic lupus erythematosus.
OS Synthetic.

Key Location/Qualifiers

FT Peptide 1..16

FT Protein /note= "hFas signal peptide"

FT /note= "mature hFas"

PN WO9601277-A1.

PD 18-JAN-1996.

PF 03-MAR-1995; 95WO-JP00349.

PR 14-FEB-1995; 95JP-0025637.

PR 06-JUL-1994; 94JP-0154706.

XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX (NISB) JAPAN TOBACCO INC.

PI Hachiya T, Noguchi J, Yonehara S;

XX WPI; 1996-087635/09.

XX N-PSDB; AAT16303.

PT Immunoassay method for soluble Fas antigen in body fluids - for
PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
PT systemic lupus erythematosus

PS Example 8; Page 49-52; 124pp; Japanese.

XX This sequence represents the sequence for the human Fas antigen contained
CC within the plasmid pCEV4/hFas. The soluble Fas antigen is included in

CC the immunoassay kit of the invention. The kit is for the assay of
CC soluble Fas antigen and contains an immobilised anti-soluble Fas
CC monoclonal antibody, as well as the standard soluble Fas antigen
CC represented by this sequence. The assay is simple and has high accuracy,
CC high sensitivity, and is capable of assaying a number of different
CC specimens at the same time. The immunoassay is used on biological
CC samples (such as serum) and is useful for diagnosis of autoimmune
CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
CC (SLE).

XX Sequence 335 AA;

SQ Query Match

Best Local Similarity 47.5%; Score 856; DB 17; Length 335;

Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

```

QY 1 MLWIAVLPLVLG-----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGGPFC 56
DB 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKTVTVTQNLGLHHDGQFCH 60
QY 57 QPCQPGKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCLCDEEHGLEVEYNCT 116
DB 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGLEVEINCT 120
QY 117 LTQNTKCKKDPDYCDSPGCEHCVRCAECHEGTLPCTATSNCRKQSPRNLMLLTL 176
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTKCKEGRSNLGLCLL 180
QY 177 VLLIPL-VFIYRKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLKSVIPIRIADM 232
DB 181 LLPIPLIIVWKRKEVQKCRKRKENQGSHPSTLPETVAINLSVDVLSKYIITIAQVM 240
QY 233 TIQEAKEFARENNIKEGIDIMHDSIODTAQKQVOLLCHWYQSHGKSDAYQDLIKGLK 292
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLK 300
QY 293 AECRRTLDKQDMQKDLGKSTPDTGNEGQCL 326
DB 301 ANLCTLAETIQTILKADITSDSENSFRNEIQSL 334

```

RESULT 14

AAW50289

ID AAW50289 standard; Protein; 335 AA.

AC AAW50289;

DT 16-JUL-1998 (first entry)

XX Human Fas antigen.

XX Human: Fas antigen; derivative; apoptosis regulation; gene therapy;
XX treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
XX apoptosis modulation.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..16

FT Peptide /label= sig_peptide

FT Peptide 17..335

FT Peptide /label= mat_peptide

FT Region 17..173

FT /note= "claimed fragment"

XX WO9742319-A1.

PN 13-NOV-1997.

XX 01-MAY-1997; 97WO-JP01502.

XX 02-MAY-1996; 96JP-0135760.

PA (MOCH) MOCHIDA PHARM CO LTD.
XX (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N;
XX WPI; 1997-558981/51.
DR N-PSDB; AAV07002.
XX FAS antigen derivative containing modified extracellular region -
PT has low antigenicity, promotes apoptosis and is useful in treatment
PT of viral and other diseases
XX Claim 2; Fig 1-2; 102pp; Japanese.
XX The present sequence was used in the development of novel Fas
CC antigen derivatives, which contain a Fas antigen extracellular
CC region lacking one or more amino acid residues in the region from
CC the amino-terminal to (but excluding) the 1st cysteine residue
CC (preferably at least 29 residues are deleted).
CC The derivatives are effective regulators of apoptosis and can be
CC used (either by administration of the polypeptide, or by the use
CC of the coding DNA in gene therapy) to treat a range of diseases,
CC e.g. diabetes, arthritis, lupus and in particular viral diseases
CC such as hepatitis, influenza and HIV, by modulating apoptosis of
CC virus-infected cells.
XX
SQ Sequence 335 AA;

Query Match 47.5%; Score 856; DB 18; Length 335;
Best Local Similarity 49.4%; Pred. No. 3.4e-62;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWTWAVLPLVLG---SQLRVHTQGTNSISESLKLRVHVDKNCSEGLYGGPFCC 56
DB 1 MLGWIITLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGHHGQGFCH 60
QY 57 QPCPGKRVKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120
QY 117 LTQNTKCKKDPDFYCDSPGCEHCVCASCEHGTLEPCTATNTNCRKQSPNRRLMLTTL 176
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNCKEGRSRLGWLCLL 180
QY 177 VLLIPL-VFIYKVRKRCWKRRDDP---ESRTSSRTIPMNASLNSLYPIRIADM 232
DB 181 LLPIPLVWVRKEVQKCRHRENOGSHESPLNPETVAINLSVDVLSKYIITIAVM 240
QY 233 TIQBAKFARENNITKEGKIDEMHDSIQDTAEQKVQLLLCWYQSHGKSDAYQDLIKGLK 292
DB 241 TLSQVKGVRKNGVNEAKIDKNDVQDTAEQKVQLLRNHLHGLGKKEAYDTLLKDLK 300
QY 293 AECRTLDKFDQVQKLGKSTPTDTGNEGOCL 326
DB 301 ANCLTAEKIQTILKIDTSDSENSFRNETQSL 334

RESULT 15
AAW49104
ID AAW49104 standard; Protein; 335 AA.
XX
AC AAW49104;
XX
DT 18-NOV-1998 (first entry)
XX
DE Fas protein.

XX Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
KW simian immunodeficiency virus; HIV; cytotoxic T lymphocyte; CTL;
XX prophylactic; AIDS.
OS Mammalia sp.

XX Key Location/Qualifiers
FH Peptide 1..16
FT /note= "Signal peptide"
FT Protein 17..335
FT /note= "Fas protein"
FT Region 17..172
FT /note= "The portion of a Fas protein which can be
FT fused to a Fc polypeptide to form a Fas-Fc
FT fusion protein"
XX WO9835692-A1.
XX 20-AUG-1998.
XX 17-FEB-1998; 98WO-GB00485.
XX 17-FEB-1997; 97GB-0003276.
XX (ISIS-) ISIS INNOVATION LTD.
XX Scream GR, Xu X;
XX WPI; 1998-456867/39.
XX N-PSDB; AAV32993.
XX Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
XX diseases - by interfering with interaction of Fas with Fas-ligand
XX expressed on activated CD4+ cells, e.g. cells infected with HIV
XX Disclosure; Fig 7; 71pp; English.
XX The present sequence represents a Fas protein sequence used in the
XX method of the invention. The method is concerned with reducing
XX depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
XX cells in an immune cell population which also comprises of Fas-ligand
XX (FasL)-expressing activated CD4+ cells. It involves contacting this
XX immune cell population with an effective amount of an agent (e.g. a
XX soluble Fas-Fc fusion protein) which would interfere with the
XX interaction between Fas and FasL. Therefore, the method is useful for
XX identifying suitable agents which can reduce depletion of activated
XX Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
XX is the use of the agent in the manufacture of therapeutic compositions.
XX Apoptosis of lymphocytes can be triggered by the interaction of the
XX cell surface receptor Fas and its ligand FasL. By interfering with
XX this interaction, the method described and its preparations can prevent
XX apoptosis of CD8+ TK lymphocytes caused by its expression of FasL on
XX activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
XX especially the result of CD4+ cell infection with an immunodeficiency
XX virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
XX virus (SIV). The claimed prevention of apoptosis may then allow
XX maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
XX towards the CD4+ cells infected with the infectious agent, enabling
XX treatment (prophylactic and/or therapeutic) of immunodeficiency
XX diseases e.g. AIDS.
SQ Sequence 335 AA;

Query Match 47.5%; Score 856; DB 19; Length 335;
Best Local Similarity 49.4%; Pred. No. 3.4e-62;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWTWAVLPLVLG---SQLRVHTQGTNSISESLKLRVHVDKNCSEGLYGGPFCC 56
DB 1 MLGWIITLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGHHGQGFCH 60
QY 57 QPCPGKRVKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120
QY 117 LTQNTKCKKDPDFYCDSPGCEHCVCASCEHGTLEPCTATNTNCRKQSPNRRLMLTTL 176
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNCKEGRSRLGWLCLL 180

QY 177 VLLIPL-VFYKYRKCWKRRQDDP---ESRTSSRETIPMNASNLSSKYIPRI AEDM 232
Db 181 LLPIPLIVVWKREVOQTCRKHKKENQGSHEPTLNPETVAINLSVDVLSKYITTTIAGYM 240
QY 233 TIQEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVOLLWCWYQSHGKSDAYODLIKGLKK 292
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDVQDTAEQKVOLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 293 AECRTLDKFDQMWOKDLGKSTPDGTGENEGQCL 326
Db 301 ANLCTLAEKIQTIIILKDITSDSENSFNRIQSL 334

Search completed: May 9, 2003, 17:05:11
Job time : 61.3354 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:03:26 ; Search time 12.8429 seconds
(without alignments)
749.153 Million cell updates/sec

Title: US-09-446-634A-23
Perfect score: 1804
Sequence: 1 MLWIWAVLPLVLGSQLRVH.....KDLGKSTPDGTGNEGOCLE 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	100.0	327	4	US-09-290-640-66
2	863.5	47.9	669	4	US-09-013-895A-3
3	863.5	47.9	669	4	US-09-448-868-3
4	856	47.5	335	2	US-08-219-237B-2
5	856	47.5	335	2	US-08-409-338-1
6	856	47.5	335	4	US-09-290-640-2
7	856	47.5	335	4	US-09-006-353A-7
8	856	47.5	335	4	US-08-468-560C-2
9	856	47.5	335	4	US-09-180-100-20
10	856	47.5	335	4	US-09-565-918-3
11	856	47.5	335	4	US-09-573-986-7
12	856	47.5	335	5	PCT-US95-17083-2
13	844	46.8	335	4	US-08-815-469-6
14	825	45.7	331	4	US-09-086-483A-3
15	810.5	44.9	314	1	US-08-444-231-19
16	810.5	44.9	314	1	US-08-152-443A-19
17	810.5	44.9	314	5	PCT-US95-17083-4
18	645	35.8	281	4	US-09-527-236A-3
19	585	32.4	219	3	US-08-974-022-45
20	585	32.4	219	4	US-08-795-445A-45
21	585	32.4	219	4	US-08-795-447A-45
22	585	32.4	219	4	US-08-974-186-45
23	585	32.4	219	4	US-08-795-446B-45
24	585	32.4	219	4	US-08-706-945D-131
25	523	29.0	167	4	US-08-828-683A-22
26	496	27.5	157	4	US-09-180-100-15
27	494.5	27.4	144	4	US-09-180-100-21

28	494.5	27.4	159	4	US-09-180-100-23	Sequence 23, Appl
29	494.5	27.4	376	4	US-09-180-100-22	Sequence 22, Appl
30	470	26.1	128	4	US-09-180-100-9	Sequence 9, Appl
31	470	26.1	143	4	US-09-180-100-10	Sequence 10, Appl
32	470	26.1	360	4	US-09-180-100-11	Sequence 11, Appl
33	462	25.6	119	4	US-08-828-683A-15	Sequence 15, Appl
34	460	25.5	119	2	US-08-219-237B-3	Sequence 3, Appl
35	460	25.5	119	4	US-08-477-347-14	Sequence 14, Appl
36	460	25.5	119	4	US-08-476-862-5	Sequence 5, Appl
37	460	25.5	119	4	US-08-468-560C-3	Sequence 3, Appl
38	305.5	16.9	149	5	PCT-US95-17083-6	Sequence 6, Appl
39	230	12.7	85	4	US-09-042-785A-26	Sequence 26, Appl
40	218	12.1	41	1	US-08-444-005-32	Sequence 32, Appl
41	215	11.9	468	4	US-09-013-895A-2	Sequence 2, Appl
42	215	11.9	468	4	US-09-565-918-2	Sequence 2, Appl
43	215	11.9	468	4	US-09-448-868-2	Sequence 2, Appl
44	214	11.9	40	1	US-08-444-005-26	Sequence 26, Appl
45	210.5	11.7	467	4	US-09-086-483A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussan, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290.640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-290-640-66

Query Match 100.0%; Score 1804; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 6.7e-158;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLWIWAVLPLVLGSQLRVHTQGTNSISLSKLRRRVHETDKNCSEGLYQGPFCCQPCQ	60
Db	1	MLWIWAVLPLVLGSQLRVHTQGTNSISLSKLRRRVHETDKNCSEGLYQGPFCCQPCQ	60
Qy	61	PGKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVTNCTLTQN	120
Db	61	PGKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVTNCTLTQN	120
Qy	121	TKCKCKDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPNRRLWLLTLVLII	180
Db	121	TKCKCKDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPNRRLWLLTLVLII	180
Qy	181	PLVFYFRYRKCKWKRRDDPESRTSRETIPMNASNLSSKYIPRTAEDMTIOEAKKF	240
Db	181	PLVFYFRYRKCKWKRRDDPESRTSRETIPMNASNLSSKYIPRTAEDMTIOEAKKF	240
Qy	241	ARENNIKEGKIDEIMHDSITQDTAEQVQLLCLWYSHGSKSDAYQDLIKGLKKAECRRITLD	300
Db	241	ARENNIKEGKIDEIMHDSITQDTAEQVQLLCLWYSHGSKSDAYQDLIKGLKKAECRRITLD	300
Qy	301	KFQDMVQKDLGKSTPDTGTGNEGOCLE	327
Db	301	KFQDMVQKDLGKSTPDTGTGNEGOCLE	327

RESULT 2
US-09-013-895A-3

Sequence 3, Application US/09013895A
Patent No. 6342363
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-013-895A-3

Query Match 47.9%; Score 863.5; DB 4; Length 669;
Best Local Similarity 49.2%; Pred. No. 4.2e-71;
Matches 164; Conservative 54; Mismatches 108; Indels 7; Gaps 2;

QY 1 MLWIAVLPVLAG----SOLRVHTQGTNSISLSKLRVRVHETDKNCSEGLYOGGPFCC 395
Db 336 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRKTIVTVETQNLGLHHDGQFCH 395
QY 57 QPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 396 KCPGPKGERKARDCTVNGDEPDCVPCQEGREYTDKAHFSKRCRCRLCDDEHGLEVEINCT 455
QY 117 LTQNTKCKKPFYCDSPGCEHCVRASCSEHGTLEPCTATSNTRKQSPRNLWLTL 176
Db 456 RTQNTKRCCKPFPNCFNSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRNLGLWCLL 515
QY 177 VLLIPLVIFYRKRRKCKWRQDDP---ESRTSSRETIPMNASLNSKYIPRAEDMT 233
Db 516 LLPIPLIVYKREVKQTCRKHKEKNGSHESPTLPETVAINLSDVLSKYITTAGVMT 575
QY 234 IQEAKKFARENKKEGKIDEIMHDSIQDTAEQVOLLCLCWYQSHGSKSDAYDLKGLKKA 293
Db 576 LSOVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHLGKKEAYDTLIDKLKKA 635
QY 294 ECRRTLDQDMVQKDLGKSTPDTGNEEGQCL 326
Db 636 NLCTLAETIQTILDKDITSDSENSFRNEIQSL 668

RESULT 3
US-09-448-868-3
Sequence 3, Application US/09448868
Patent No. 6461823
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 27-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-868-3

Query Match 47.9%; Score 863.5; DB 4; Length 669;
Best Local Similarity 49.2%; Pred. No. 4.2e-71;
Matches 164; Conservative 54; Mismatches 108; Indels 7; Gaps 2;

QY 1 MLWIAVLPVLAG----SOLRVHTQGTNSISLSKLRVRVHETDKNCSEGLYOGGPFCC 395
Db 336 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRKTIVTVETQNLGLHHDGQFCH 395
QY 57 QPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 396 KCPGPKGERKARDCTVNGDEPDCVPCQEGREYTDKAHFSKRCRCRLCDDEHGLEVEINCT 455
QY 117 LTQNTKCKKPFYCDSPGCEHCVRASCSEHGTLEPCTATSNTRKQSPRNLWLTL 176
Db 456 RTQNTKRCCKPFPNCFNSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRNLGLWCLL 515
QY 177 VLLIPLVIFYRKRRKCKWRQDDP---ESRTSSRETIPMNASLNSKYIPRAEDMT 233
Db 516 LLPIPLIVYKREVKQTCRKHKEKNGSHESPTLPETVAINLSDVLSKYITTAGVMT 575
QY 234 IQEAKKFARENKKEGKIDEIMHDSIQDTAEQVOLLCLCWYQSHGSKSDAYDLKGLKKA 293
Db 576 LSOVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHLGKKEAYDTLIDKLKKA 635

QY	294	ECRTFLDKFQDMQKDLGKSPDPTGNEGQCL	326
Db	636	NLCTLAEXIQTIILKDTSDSENSFRNEIQSL	668
RESULT 4			
US-08-219-237B-2			
: Sequence 2, Application US/08219237B			
: Patent No. 5874546			
: GENERAL INFORMATION:			
: APPLICANT: NAGATA, Shigekazu			
: APPLICANT: ITOH, Naoto			
: APPLICANT: YONEHARA, Shin			
: TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen			
: NUMBER OF SEQUENCES: 11			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: James W. Hellwege			
: STREET: P.O. Box 2266 Eads Station			
: CITY: Arlington			
: STATE: Virginia			
: COUNTRY: USA			
: ZIP: 22202			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patent in Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/219,237B			
: FILING DATE: 28-MAR-1994			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/872,129			
: FILING DATE: 22-APR-1992			
: CLASSIFICATION: 435			
: ATTORNEY/AGENT INFORMATION:			
: NAME: James W. Hellwege			
: REGISTRATION NUMBER: 28,808			
: REFERENCE/DOCKET NUMBER: 516762			
: INFORMATION FOR SEQ ID NO: 2:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 335 amino acids			
: TYPE: amino acid			
: TOPOLOGY: linear			
: MOLECULE TYPE: protein			
US-08-219-237B-2			
Query Match 47.5%; Score 856; DB 2; Length 335;			
Best Local Similarity 49.4%; Pred. No. 8.3e-71;			
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;			
QY	1	MLHTWAVLPVLAG-----SQLRVHTQGNISSESLKLRARRVHETDKNCSEGLYQGPFCC	56
Db	1	MLGWTLPVLTVSARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH	60
QY	57	QPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVTNCT	116
Db	61	KPCPPGKARDCTVNGDEPCVPCQEGKEYTDKRAHFSKRCRCLDDEHGLEVEINCT	120
QY	117	LTQNTKCKKPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPRNLMLTTL	176
Db	121	RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLGLCLL	180
QY	177	VLLIPL-VFYIRKVRKRCWKRRQDDP---BSRTSSRTIPMNASNLSSKYIPRAEDM	232
Db	181	LLPIPLVWVRKVEQKTCRKHRENQGSHPSTLNPTVAINLSDVLSKYITITAGVM	240
QY	233	TIQAKKFARENNIKEGKIDETIMHDSIODTAQOKVOLLCLWQSHGKSDAYODLKLKK	292
Db	241	TLQVKGFVRKNGVNEAKIDKINDVNDVDTTQNTTQNTTQNTTQNTTQNTTQNTTQNTT	300
QY	293	ACRRTLDKFDQMDQKDLGKSPDPTGNEGQCL	326

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QY 177 VLLIPL-VFIYKVRKRCWKRRRODDP- --ESRSTSSRETIPMNASNLSKYIPRIADM 232
Db 181 LLIPLIIVWVRKKEVQKTCRKHREKENGSHESPTLAPETVAIINLSDVDLSKYITTIAGVM 240
QY 233 TIOEAKKEARENNIKEGKIDEIMHDSIQDTAEQKVOLLCKVQSHGSKSDAYODLKGKK 292
Db 241 TILSQVKGVRKNGVNEAKIDEIKNVNDVQDTAEQKVOLLRNWHLQHGKKEAYDTLKLDKKK 300
QY 293 AECRRITDKDFQDMQVKDLGKSTPDTGNEGQCL 326
Db 301 ANLCTLAEKIQIITLKDITSDSENSFRNEIQSL 334

RESULT 6
US-09-290-640-2
; Sequence 2, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-640-2

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Query Match	47.5%;	Score 856;	DB 4;	Length 335;
Best Local Similarity	49.4%;	Pred. No. 8.3e-71;		
Matches 165;	Conservative 54;	Mismatches 107;	Indels 8;	Gaps 3
QY	1	MLMWAVLPLVLG----	SQLRVHTQGNISIS	KLURRVHETDKNCSEGLYQGGPFCC 56
Db	1	MLGIWTLPLVLT	SVARUSSVNAQVYTDINSKGLERLKT	VTVETQNLBGLHHDGQFCH 60
QY	57	QPCQPGKKVVEDCKMNGGTP	CACTEGCKEYMDKNHYADCKRCTL	CDEHGLEVEINCT 116
Db	61	KCPGPGERKARDCTVNGDEP	CDVCPQEGKEYTDKAHESKCR	CRRCRJCDEHGLEVEINCT 111
QY	117	LTONTKCKCKDPFYCDSPG	CEHCYVRCASCHGTLPECTAT	SNTNCRKQSPRNLWTLT 176
Db	121	RFONTCKCKPNFCNFTVC	DEHDPCTCKCEHGIKECTLT	SNTNCKEGRSRNLGWLCL 180
QY	177	VLLIPL-VFIYKRYKRCWK	RKRRDDP----	ESKTSSERETIPMNASLSKYIPRAEDM 232
Db	181	LLPIPLIIVVVRKEVQK	TKRHKENGSGHESPTLPET	VAINLSVDLSKYITTAGVM 240
QY	233	TIQEAKEFARNNTKEG	IDEIMHDSITQDTAEQVOLL	CWYOSHGSKDAYODLKGKK 292
Db	241	TLISQVKGFRKNGVNEAK	IDEIKNDNVQDTAEQVOLL	RNHWQLHGKKEAYDTLKDULK 300
QY	293	ACERRTLDKQDMQKDLG	KSTPDTGNEGQCL 326	
Db	301	ANLCTLAEKIITILK	DITSSENSFRNEIQL 334	

RESULT 7
US-09-006-353A-7
; Sequence 7, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
;

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-353A-7

Query Match	47.5%	Score 856;	DB 4;	Length 335;
Best Local Similarity:	49.4%			

Qy	1	MLWIAVLPLVL	AG----	SQLRVHTQGTNSISELKLRRRVHETDKNCSEGLYOGGFPCC	56
Db	1	MLGIWTLLPLVL	TSVARLSKSVNAQ	YTDINSKGLELRKVTVTYVETQNLBSLHHDGQFCH	60
Qy	57	OPCOPGKKVEDCK	MNGGTPTCAPCT	EGKYMDKNHYADKRCRCTCDEBHGLEVEINCT	116
Db	61	KPCPPGERKARDCT	VNGDEPDCVQ	BGKEYTDKAHFSKRCRCLDEBHGLEVEINCT	120
Qy	117	LTQNTCKCKAPDF	YCDSPGCEHCVR	CASCEHGLETPCTATSNTRCKQSPNRNLWLTIL	176
Db	121	RTQNTCKRCAPNF	CFNCSTVCEHC	DPCTCBHGIIKECTLSNTKCBEGSRNLGLWLCLL	180
Qy	177	VLLIPL-VFYIRY	KRYRKCKWKRR	QDDP---ESRTSSRETIPMASNLSLSKYIPRAEDM	232
Db	181	LLDPLIVWVKRE	VQKTCRKHKEN	QSGSHESFTLPETVAIINLSVDVLSKYITTTAGVM	240
Qy	233	TIOEAKKFAREN	NKGGKIDEIMH	DSIQDTAEQKVQLLCCWYQSHGKSDAYODLIKGLKK	292
Db	241	TLSDQVGFVRK	NGVNEAKIDEI	KNDNVQDTAEQKVOLLRNWHLHGKKEAYDTLIRKDLKK	300
Qy	293	AECCRTLDREF	QDMVQDKLGS	PTDPDTGNEGQCL	326
Db	301	ANLCTLAEKI	QTIILKDLT	SDSENSFRNEIOSL	334

RESULT 8
US-08-468-560C-2
; Sequence 2, Application US/08468560C
; Patent No. 6270998
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.

STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-560C-2

Query Match 47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWIAVLPVLAG----SQLRVHTQGTNSISLKLRRRHVETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLERKTKTTVETQNLGLHHDGQFCH 60
QY 57 QPCQPKKKVDECKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHSSKRCRCLDEGHGLEVEINCT 120
QY 117 LTQNTKCKKPDFCYCDSPGCEHCVRASCENGHTLEPCATNTNCRKQSPNRRLWLITL 176
DB 121 RTQNTKCRCKPNFECSTVCEHCDCPTCKEHHIIECTLTSTNCKKEGSRSLGLWCLL 180
QY 177 VLLIPL-VFYIRKYRKRKWKRRDDP---ESRTSSRETIPMNASLNSLYIPRIADM 232
DB 181 LLPIPLVWKRKEVQTCRKHKENOGSHESPTLNPTETVAINLSVDLSKIYITTIAGVM 240
QY 233 TIQAKKFARENNIKEGKIDIMHDSIQDTAEQVQLLLCWYQSHGKSDAYQDLIKGLKK 292
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDVQDTAEQVQLLRNHNHQLHGKKEAYDTLIKDLKK 300
QY 293 AECDRTLDKQDMVQKDLGKSTPTDGNENEGCQL 326
DB 301 ANLCTLAETIQTILKIDTSSENSNFRNIQSL 334

RESULT 9
US-09-180-100-20
Sequence 20, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAKAMURA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 20
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-20

Query Match 47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWIAVLPVLAG----SQLRVHTQGTNSISLKLRRRHVETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLERKTKTTVETQNLGLHHDGQFCH 60

QY 57 QPCQPKKKVDECKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHSSKRCRCLDEGHGLEVEINCT 120
QY 117 LTQNTKCKKPDFCYCDSPGCEHCVRASCENGHTLEPCATNTNCRKQSPNRRLWLITL 176
DB 121 RTQNTKCRCKPNFECSTVCEHCDCPTCKEHHIIECTLTSTNCKKEGSRSLGLWCLL 180
QY 177 VLLIPL-VFYIRKYRKRKWKRRDDP---ESRTSSRETIPMNASLNSLYIPRIADM 232
DB 181 LLPIPLVWKRKEVQTCRKHKENOGSHESPTLNPTETVAINLSVDLSKIYITTIAGVM 240
QY 233 TIQAKKFARENNIKEGKIDIMHDSIQDTAEQVQLLLCWYQSHGKSDAYQDLIKGLKK 292
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDVQDTAEQVQLLRNHNHQLHGKKEAYDTLIKDLKK 300
QY 293 AECDRTLDKQDMVQKDLGKSTPTDGNENEGCQL 326
DB 301 ANLCTLAETIQTILKIDTSSENSNFRNIQSL 334

RESULT 10
US-09-565-918-3
Sequence 3, Application US/09565918
Patent No. 6433147
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT APPLICATION NUMBER: US/09/565,918
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-918-3

Query Match 47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLWIAVLPVLAG----SQLRVHTQGTNSISLKLRRRHVETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLERKTKTTVETQNLGLHHDGQFCH 60

```

; Sequence 2, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17083-2

Query Match 47.5%; Score 856; DB 5; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWVLPVLAG----SQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPFCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60

QY 57 QPCPGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 1 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120

QY 117 LTQNTCKCKPFDYCDSPGCEHCVRCAHGTLEPCTATNTNCRKQSPRNLWLLTIL 176
Db 1 RTQNTCKRCRPNFNCSTVCEHCDPCTCKEHIKECTITNTNCKEESRNLGLWLCUL 180

QY 177 VLLIPL-VFIYRKRYKRCWKRRQDDP---ESRTSSRETIPMNASLSKYIPRIAEDM 232
Db 181 LLPIPLVWVKRQVKTCKRKRNQOGSHESPTLNPTVAINLSDVLSKYITTIAGVM 240

QY 233 TIOEAKKFARENNIKEGKIDETWHDSDIOTABQKVLQLLCWYQSHGKSDAYQDLIKGLKK 292
Db 241 TLSQVKGFRKNGVNEAKIDEKNDVQDTAEQVOLLRNHQLHGKKEAYDTLIKDLKK 300

QY 293 ACERTLQKFDQVMDLGSPPDTGNEGQCL 326
Db 301 ANLCTLAEKIQTILKDIITSDSENSNFRNEIQSL 334

RESULT 11
US-09-573-986-7
; Sequence 7, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-7

Query Match 47.5%; Score 856; DB 4; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWVLPVLAG----SQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPFCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60

QY 57 QPCPGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 1 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120

QY 117 LTQNTCKCKPFDYCDSPGCEHCVRCAHGTLEPCTATNTNCRKQSPRNLWLLTIL 176
Db 1 RTQNTCKRCRPNFNCSTVCEHCDPCTCKEHIKECTITNTNCKEESRNLGLWLCUL 180

QY 177 VLLIPL-VFIYRKRYKRCWKRRQDDP---ESRTSSRETIPMNASLSKYIPRIAEDM 232
Db 181 LLPIPLVWVKRQVKTCKRKRNQOGSHESPTLNPTVAINLSDVLSKYITTIAGVM 240

QY 233 TIOEAKKFARENNIKEGKIDETWHDSDIOTABQKVLQLLCWYQSHGKSDAYQDLIKGLKK 292
Db 241 TLSQVKGFRKNGVNEAKIDEKNDVQDTAEQVOLLRNHQLHGKKEAYDTLIKDLKK 300

QY 293 ACERTLQKFDQVMDLGSPPDTGNEGQCL 326
Db 301 ANLCTLAEKIQTILKDIITSDSENSNFRNEIQSL 334

RESULT 12
PCT-US95-17083-2
```

```

; Sequence 2, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17083-2

Query Match 47.5%; Score 856; DB 5; Length 335;
Best Local Similarity 49.4%; Pred. No. 8.3e-71;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWVLPVLAG----SQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPFCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETQNLGLHHDGQFCH 60

QY 57 QPCPGKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 1 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCRLCDDEHGLEVEINCT 120

QY 117 LTQNTCKCKPFDYCDSPGCEHCVRCAHGTLEPCTATNTNCRKQSPRNLWLLTIL 176
Db 1 RTQNTCKRCRPNFNCSTVCEHCDPCTCKEHIKECTITNTNCKEESRNLGLWLCUL 180

QY 177 VLLIPL-VFIYRKRYKRCWKRRQDDP---ESRTSSRETIPMNASLSKYIPRIAEDM 232
Db 181 LLPIPLVWVKRQVKTCKRKRNQOGSHESPTLNPTVAINLSDVLSKYITTIAGVM 240

QY 233 TIOEAKKFARENNIKEGKIDETWHDSDIOTABQKVLQLLCWYQSHGKSDAYQDLIKGLKK 292
Db 241 TLSQVKGFRKNGVNEAKIDEKNDVQDTAEQVOLLRNHQLHGKKEAYDTLIKDLKK 300

QY 293 ACERTLQKFDQVMDLGSPPDTGNEGQCL 326
Db 301 ANLCTLAEKIQTILKDIITSDSENSNFRNEIQSL 334

RESULT 13
US-08-815-469-6
; Sequence 6, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIORITY APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-6

Query Match 46.8%; Score 844; DB 4; Length 335;
Best Local Similarity 49.1%; Pred. No. 1.1e-69;
Matches 164; Conservative 54; Mismatches 108; Indels 8; Gaps 3;

QY 1 MLWTAVLPLVLG----SQLRVHTQGTNSISESLKRRRVHETDKNCEGLYQGPPCC 56
DB 1 MGLTWLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 57 QPCPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRTCLDCEHGLEVEYNCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEHGLEVEINCT 120
QY 117 LTQNTKCKKPDFCYDSPGCEHCVRCAECHEGTLEPCATNTNCRKOSPRLNLLTIL 176
DB 121 RTQNTKCKCKNFNFONSTVCEHCPCTKCEHGIIEKCTLTNTKCEGSRNLGLWCLL 180
QY 177 VLLIPL-VFIYKRYKRRKCRRRDDP---ESRTSSRETIPMNASNLSKYIPRIADM 232
DB 181 LLPIPLIWWKRVKQKTCRHRKENGSHESPTLNPTVAINLSDVDLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYODLIKGLK 292
DB 241 TLSQVKGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHHQLHGKKEAYDTLIKDLK 300
QY 293 AECRRLDKFQDMVKDGLGSTPDTGNENEGOCL 326
DB 301 ANLCTAEKIQTILKIDTSDSENSNFRNEIQSL 334

RESULT 14
US-09-086-483A-3
Sequence 3, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/086,483A
APPLICATION NUMBER: 60/050,936
FILING DATE: May-30-97
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-483A-3

Query Match 45.7%; Score 825; DB 4; Length 331;
Best Local Similarity 49.9%; Pred. No. 5.7e-68;
Matches 167; Conservative 53; Mismatches 101; Indels 14; Gaps 8;

QY 1 MLWTAVLPLVLG----SQLRVHTQGTNSISESLKRRRVHETDKNCEGLYQGPPCC 56
DB 1 MGLTWLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNL-EGLHHDGQF-C 58
QY 57 QPCPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRTCLDCEHGLEVEYNCT 116
DB 59 HPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEHGLEVEINCT 118
QY 117 LTQNTKCKKPDFCYDSPGCEHCVRCAECHEGTLEPCATNTNCRKOSPRLNLLTIL 176
DB 119 RTQNTKCKCKNFNFONSTVCEHCPCTKCEHGIIEKCTLTNTKCEGSRNNGW-LCLL 177
QY 177 VLLIPL-VFIYKRYKRRKCRRRDDP---ESRTSSRETIPMNASNLSKYIPRIADM 232
DB 178 LLPIPLIWWKRVKQKTCRHRKENGSHESPTLNPTVAINLSDVDLSKYITTIAGVM 237
QY 233 TIOEAKKFARENNIKEGKIDEIMHDSIQDTAEQKVQLLLCWYQSHGKSDAYODLIKGLK 292
DB 238 TLSQVKGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHHQLHGKKEAYDTLIKDLK 297
QY 293 AE-CRRTLDKFDQDMVKDGLGSTPDTGNENEGOCL 326
DB 298 ANLC--TLAEKTIILKIDTSDSENSNFRNEIQSL 330

RESULT 15
US-08-444-231-19
Sequence 19, Application US/08444231
Patent No. 5652210
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-231-19

Query Match 44.9%; Score 810.5; DB 1; Length 314;
Best Local Similarity 46.8%; Pred. No. 1.2e-66;
Matches 156; Conservative 50; Mismatches 100; Indels 27; Gaps 3;
QY 1 MLWIAVLPVLAG-----SOLRVHTQNTSISLSKLRVRVHETDKNCSEGLYQGGPFCC 56
Db 1 MLGIWTLPLVLTAVARLSKSVNAQVTDINSKGLERKVTVTVEIQNLSEGLHHDGQFCH 60
QY 57 QPCQPKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCITCDEHGLEVEINCT 116
Db 61 KPCPPGERKARDTVNGDEPCVQEGREYTDKAHFSSKRCRCRLCDEHGLEVEINCT 120
QY 117 LTQNTCKCKPDPYCDSPGCEHCVCASCSEHGTLEPCTATSNCRKQSPRNLWLLTIL 176
Db 121 RTQNTKRCCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEE----- 168
QY 177 VLLIPLVFIYKRYKRCCKWRRODDP---ESRTSSRETIPMNASNLISKYIPRIADMT 233
Db 169 -----VKREVKQTCRKHREKNOGSHESPTLNPTVAINLSDVDLSKYITTIAGVMT 220
QY 234 IQEAKFARENKKEKIDIMHDSIQDTAOKVQLLCWYQSHGKSDAYQDLIKLKA 293
Db 221 LSQVKGFRKNGVNEAKIDEIKNDVODFAOKVQLLRNWHQHLHGKKEAYDLIKLKA 280
QY 294 ECRRLDKFDQVMVQDKLGKSTPDTGNENEGQCL 326
Db 281 NLCTLAEKIQTIIKIDITSSENSFNEIQSL 313

Search completed: May 9, 2003, 17:08:25
Job time : 13.8429 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:05:23 ; Search time 16.3006 seconds
(without alignments)
1846.092 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIAVLPVLVLAGSQLRVH.....KDLGKSTPDGTGNEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1804	100.0	327	10	US-09-802-669-66
2	1166	64.6	204	10	US-09-948-018-18
3	863.5	47.9	669	9	US-10-226-296-3
4	863.5	47.9	669	9	US-10-226-318-3
5	856	47.5	335	10	US-09-826-212-7
6	856	47.5	335	10	US-09-802-669-2
7	856	47.5	335	10	US-09-949-713-20
8	856	47.5	335	10	US-09-874-138-4
9	856	47.5	335	10	US-09-884-987-2
10	856	47.5	335	10	US-09-935-727-9
11	856	47.5	335	12	US-10-005-842-4
12	844	46.8	335	9	US-09-314-889-6
13	844	46.8	335	10	US-09-333-966-6
14	645	35.8	281	9	US-09-756-854-3
15	645	35.8	281	9	US-10-041-574-3
16	523	29.0	167	9	US-10-112-793-22
17	523	29.0	237	9	US-09-925-299-960
18	523	29.0	237	10	US-09-925-299-960
19	496	27.5	157	10	US-09-949-713-15

20	494.5	27.4	144	10	US-09-949-713-21	Sequence 21, Appl
21	494.5	27.4	159	10	US-09-949-713-23	Sequence 23, Appl
22	494.5	27.4	376	10	US-09-949-713-22	Sequence 22, Appl
23	470	26.1	128	10	US-09-949-713-9	Sequence 9, Appl
24	470	26.1	143	10	US-09-949-713-10	Sequence 10, Appl
25	470	26.1	360	10	US-09-949-713-11	Sequence 11, Appl
26	462	25.6	119	9	US-10-112-793-15	Sequence 15, Appl
27	460	25.5	119	10	US-09-800-909-5	Sequence 5, Appl
28	460	25.5	119	10	US-09-884-987-3	Sequence 3, Appl
29	460	25.5	119	10	US-09-800-908-14	Sequence 14, Appl
30	215	11.9	418	9	US-09-992-964-14	Sequence 14, Appl
31	215	11.9	418	10	US-09-887-879-14	Sequence 2, Appl
32	215	11.9	468	9	US-10-226-296-2	Sequence 2, Appl
33	215	11.9	468	9	US-10-226-318-2	Sequence 2, Appl
34	215	11.9	468	12	US-10-039-785-1	Sequence 1, Appl
35	209	11.6	77	9	US-10-112-793-24	Sequence 24, Appl
36	205	11.4	148	10	US-09-855-266A-2	Sequence 2, Appl
37	205	11.4	176	10	US-09-855-266A-1	Sequence 1, Appl
38	205	11.4	283	10	US-09-924-231-2	Sequence 2, Appl
39	205	11.4	283	10	US-09-934-289A-13	Sequence 13, Appl
40	205	11.4	283	10	US-09-935-727-31	Sequence 31, Appl
41	205	11.4	283	12	US-10-020-787-2	Sequence 2, Appl
42	204	11.3	283	12	US-10-066-209-2	Sequence 2, Appl
43	202	11.2	77	9	US-09-992-964-17	Sequence 17, Appl
44	202	11.2	77	10	US-09-887-879-17	Sequence 17, Appl
45	202	11.2	272	10	US-09-782-980-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-802-669-66
; Sequence 66, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Marcussan, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802.669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-669-66

Query Match	100.0%	Score 1804	DB 10	Length 327
Best Local Similarity	100.0%	Pred. No. 8.6e-125		
Matches 327	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MLWIAVLPVLVLAGSQLRVHQTGNTSISLKLRRRVHETDKNCSEGLYQGGPFCQPCQ	60	
Db	1	MLWIAVLPVLVLAGSQLRVHQTGNTSISLKLRRRVHETDKNCSEGLYQGGPFCQPCQ	60	
Qy	61	PGKKVDECKNMGTTTCAPCTEGKEYMDKNHYADKRCRRLCDDEHGLEVETNCTLTON	120	
Db	61	PGKKVDECKNMGTTTCAPCTEGKEYMDKNHYADKRCRRLCDDEHGLEVETNCTLTON	120	
Qy	121	TKCKCKPFDYCDSPGCEHVCRCASCEHGTLEPCTATSTNTNCRKQSPRNLWLLTLLVLLI	180	
Db	121	TKCKCKPFDYCDSPGCEHVCRCASCEHGTLEPCTATSTNTNCRKQSPRNLWLLTLLVLLI	180	
Qy	181	PLVFYIKYRKRKCKWRQDDPESRTSSRETIPMNASNLSLSKYIPRIAEDWTIOEAKKF	240	

Db 181 PLVFIYKRYKRCWKRRQDDPSRTSSRETIPNANSLSLSKYIPRIADMTIQEAKF 240
QY 241 ARENNIKEGIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLLKGLKAECCRTLD 300
Db 241 ARENNIKEGIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLLKGLKAECCRTLD 300
QY 301 KFDQMVQKDLGKSTPDGTGNEGQCLE 327
Db 301 KFDQMVQKDLGKSTPDGTGNEGQCLE 327

RESULT 2
US-09-948-018-18
; Sequence 18, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-948-018-18

Query Match 64.6%; Score 1166; DB 10; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.8e-78;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWIWAVPLVLVLAGSOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPFCQPCQ 60
Db 1 MLWIWAVPLVLVLAGSOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPFCQPCQ 60

QY 61 PGKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCLCDEHGLEVEINCTLTQN 120
Db 61 PGKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCLCDEHGLEVEINCTLTQN 120

QY 121 TKCKKAPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPNRRLWLLTILVLLI 180
Db 121 TKCKKAPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPNRRLWLLTILVLLI 180

QY 181 PLVFIYKRYKRCWKRRQDDPS 204
Db 181 PLVFIYKRYKRCWKRRQDDPS 204

RESULT 3
US-10-226-296-3
; Sequence 3, Application US/10226296
; Publication No. US20030036168A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US

; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,296
; FILING DATE: 23-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-226-296-3

Query Match 47.9%; Score 863.5; DB 9; Length 669;
Best Local Similarity 49.2%; Pred. No. 1.5e-55;
Matches 164; Conservative 54; Mismatches 108; Indels 7; Gaps 2;

QY 1 MLWIWAVPLVLVLAGSOLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPFCQ 56
Db 336 MLGIWTLPLVLVLTAVRLSKSVNAQVTDINSKGLERKTVTTVETQNLGLHHDGQFCH 395

QY 57 QPCQPKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCLCDEHGLEVEINCT 116
Db 396 KCPGGERKARCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEHGLEVEINCT 455

QY 117 LTQNTKCKKPPDFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKQSPNRRLWLLTIL 176
Db 456 RTQNTKCRCKPFPFCSTVCEHCDCPCKCEHGIKECTLTSTNTCKCEGSRNLGLCLL 515

QY 177 VLLIPLVFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLSSKYIPRIADMT 233
Db 516 LLPIPLVFIYKRYKRCWKRRQDDPSPTNPETVAINLSVDLSKYITTIAGVMT 575

QY 234 IQEAKKFARENNIKEGIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLLKGLKKA 293
Db 576 LSQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQKQVOLLRNHQLHKGKKEAYDTLIKDLKKA 635

QY 294 ECRRLDKFDQMVQKDLGKSTPDGTGNEGQCCL 326
Db 636 NLCTLAETQITILKDLTSDSENSFNRIQSL 668

RESULT 4
US-10-226-318-3
; Sequence 3, Application US/10226318
; Publication No. US20030073187A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; Receptor 4), Member of the TNF-Receptor

Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

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QY 1 MLWIWAVLPVLVLAG-----SOLRVHTQGTNSISESLKRRRVHETDKNCSEGLYOGGPCC 56
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Db 1 MLCIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60

QY 57 OPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
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Db 61 KCPGPERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEHGLEVEINCT 120

QY 117 LTQNTKCKKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPRNLWLLTIL 176
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Db 121 RTQNTKCKKPNFCNVTCEHCDPCTKCEHGIKECTLTNTCKEBSRNLGWLCLL 180

QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLSKIYIPRIADM 232
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Db 181 LLPIPLIWWKRVKQVTCRKRKENQGSHPETLNPETVAINLSVDLSKIYITTIAGVM 240

QY 233 TIOEAKKFARENNIKEGKIDEMHDSIQDTAEQVQLLWCYQSHGSKSDAYODLIGLKK 292
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Db 241 TISOVKGFVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300

QY 293 AECRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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Db 301 ANLCTLAETIQTILKDIITSDSENSFRNEIQSL 334
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RESULT 7

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US-09-949-713-20
; Sequence 20, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. US20020044944A1io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-20
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Query Match 47.5%; Score 856; DB 10; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWAVLPVLVLAG-----SOLRVHTQGTNSISESLKRRRVHETDKNCSEGLYOGGPCC 56
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Db 1 MLCIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60

QY 57 OPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KCPGPERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEHGLEVEINCT 120

QY 117 LTQNTKCKKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPRNLWLLTIL 176
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 RTQNTKCKKPNFCNVTCEHCDPCTKCEHGIKECTLTNTCKEBSRNLGWLCLL 180

QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLSKIYIPRIADM 232
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LLPIPLIWWKRVKQVTCRKRKENQGSHPETLNPETVAINLSVDLSKIYITTIAGVM 240

QY 233 TIOEAKKFARENNIKEGKIDEMHDSIQDTAEQVQLLWCYQSHGSKSDAYODLIGLKK 292
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Db 241 TISOVKGFVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300
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RESULT 9

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US-09-884-987-2
; Sequence 2, Application US/09884987
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QY 293 AECRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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Db 301 ANLCTLAETIQTILKDIITSDSENSFRNEIQSL 334

RESULT 8
US-09-874-138-4
; Sequence 4, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/1148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-4
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Query Match 47.5%; Score 856; DB 10; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWAVLPVLVLAG-----SOLRVHTQGTNSISESLKRRRVHETDKNCSEGLYOGGPCC 56
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Db 1 MLCIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60

QY 57 OPCQPKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KCPGPERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEHGLEVEINCT 120

QY 117 LTQNTKCKKPDFYCDSPGCEHCVRCAECHEGTLEPCTATNTNCRKQSPRNLWLLTIL 176
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Db 121 RTQNTKCKKPNFCNVTCEHCDPCTKCEHGIKECTLTNTCKEBSRNLGWLCLL 180

QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP---ESRTSSRETIPMNASNLSKIYIPRIADM 232
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Db 181 LLPIPLIWWKRVKQVTCRKRKENQGSHPETLNPETVAINLSVDLSKIYITTIAGVM 240

QY 233 TIOEAKKFARENNIKEGKIDEMHDSIQDTAEQVQLLWCYQSHGSKSDAYODLIGLKK 292
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TISOVKGFVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300

QY 293 AECRTLDKFQDMVQKDLGKSTPDTGNENEGQCL 326
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Db 301 ANLCTLAETIQTILKDIITSDSENSFRNEIQSL 334
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Patent No. US20020102653A1
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigetazu et al
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-987-2

Query Match 47.5%; Score 856; DB 10; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWVLPVLAG----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGGPCC 56
DB 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCQGGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCLCDEEHGLEVETNCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGLEVETNCT 120
QY 117 LTQNTKCKKPDFCYDCSPGCEHCVCASCEHGTLEPCTATSNCRKQSPNRLLWLLTIL 176
DB 121 RTQNTKCKCKPNFFCNSTVCEHCDPCTKEGIIKECTLTSTNCKEGRSNLWGLCLL 180
QY 177 VLLIPL-VFIYRKRYKRCWKRRRDDP---ESRTSSRETIPMNASLNSISKYIPRIAEDM 232
DB 181 LLPIPLIIVWVRKKEVQKTCRKHRENQSHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNIEGKIDETIMHDSIODTAQKVOLLWCYQSHGKSDAYODLIKGLKK 292
DB 241 TLSQVKGVRKNGVNEAKIDEIKNDVQDTAEQKVOLLRNHQLHKGKAYDTLIKDLKK 300
QY 293 AECRTLTOKFQDMVOKLGKSTPDTGNEGQCL 326
DB 301 ANLCTLAEKIQTIIILKDTSDSENSFNRIQSL 334

RESULT 10
US-09-935-727-9
Sequence 9, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774

PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-727-9

Query Match 47.5%; Score 856; DB 10; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIWVLPVLAG----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGGPCC 56
DB 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCQGGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCLCDEEHGLEVETNCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDEGHGLEVETNCT 120
QY 117 LTQNTKCKKPDFCYDCSPGCEHCVCASCEHGTLEPCTATSNCRKQSPNRLLWLLTIL 176
DB 121 RTQNTKCKCKPNFFCNSTVCEHCDPCTKEGIIKECTLTSTNCKEGRSNLWGLCLL 180
QY 177 VLLIPL-VFIYRKRYKRCWKRRRDDP---ESRTSSRETIPMNASLNSISKYIPRIAEDM 232
DB 181 LLPIPLIIVWVRKKEVQKTCRKHRENQSHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
QY 233 TIOEAKKFARENNIEGKIDETIMHDSIODTAQKVOLLWCYQSHGKSDAYODLIKGLKK 292
DB 241 TLSQVKGVRKNGVNEAKIDEIKNDVQDTAEQKVOLLRNHQLHKGKAYDTLIKDLKK 300
QY 293 AECRTLTOKFQDMVOKLGKSTPDTGNEGQCL 326
DB 301 ANLCTLAEKIQTIIILKDTSDSENSFNRIQSL 334

RESULT 11
US-10-005-842-4
Sequence 4, Application US/10005842
Patent No. US20020098550A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Su, Jeffrey
Rosen, Craig A.
TITLE OF INVENTION: Death Domain Containing Receptor 5
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,583
FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEFAX: 3013098439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-005-842-4
Query Match 47.5%; Score 856; DB 12; Length 335;
Best Local Similarity 49.4%; Pred. No. 2.5e-55;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MLWIAVLPLVLG----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCQPGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKRAHFSKRCRCLCDDEHGLEVEINCT 120
QY 117 LTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 176
DB 121 RTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 180
QY 177 VLLIPL-VFIVYKVRKCKWRKRRDDP---ESRTSSRETIPMNASLSKYIPRIADM 232
DB 181 LLPIPLVWVRKKEVQKTCRKRKENGSHESPTLNPTVAINLSVDLSKYITTIAGVM 240
QY 233 TIOEAKKFARENKKEGKIDIMHDSIQDTAEQVQLLWYQSHGSKSDAYQDLIKGLKK 292
DB 241 TISQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQVQLLRNWHQHLGKKEAYDTLIKDLKK 300
QY 293 AECRRRLDKFQDMVQKDLGKSTPDTGNEGQCL 326
DB 301 ANLCTLAETIQTILKIDITSSENSFRNEIQSL 334

RESULT 12
US-09-314-889-6
Sequence 6, Application US/09314889
Publication No. US20030077694A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/314,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/815,469
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-314-889-6

Query Match 46.8%; Score 844; DB 9; Length 335;
Best Local Similarity 49.1%; Pred. No. 1.9e-54;
Matches 164; Conservative 54; Mismatches 108; Indels 8; Gaps 3;

QY 1 MLWIAVLPLVLG----SQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPPCC 56
DB 1 MLGIWTLPLVLTSLVRLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
QY 57 QPCQPGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKRAHFSKRCRCLCDDEHGLEVEINCT 120
QY 117 LTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 176
DB 121 RTQNTKCKPDPFYCDSPGCEHCVRCAEHTLEPCATNTNCRKQSPRNLWLLTIL 180
QY 177 VLLIPL-VFIVYKVRKCKWRKRRDDP---ESRTSSRETIPMNASLSKYIPRIADM 232
DB 181 LLPIPLVWVRKKEVQKTCRKRKENGSHESPTLNPTVAINLSVDLSKYITTIAGVM 240
QY 233 TIOEAKKFARENKKEGKIDIMHDSIQDTAEQVQLLWYQSHGSKSDAYQDLIKGLKK 292
DB 241 TISQVKGFEVRKNGVNEAKIDEIKNDVQDTAEQVQLLRNWHQHLGKKEAYDTLIKDLKK 300
QY 293 AECRRRLDKFQDMVQKDLGKSTPDTGNEGQCL 326
DB 301 ANLCTLAETIQTILKIDITSSENSFRNEIQSL 334

RESULT 13
US-09-333-966-6
Sequence 6, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington

APPLICANT: Ni, Jian
 Yu, Guo-Liang
 Fan, Ping
 Gentz, Reiner
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TF9
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release 1.0, Version 1.30
 CURRENT APPLICATION DATA: US/09/756,854
 APPLICATION NUMBER: US/09/756,854
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/095,094
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kenley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PF375
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-756-854-3

```

Query Match      35.88; Score 645; DB 9; Length 281;
Best Local Similarity 45.6%; Pred. No. 5.8e-40;
Matches 128; Conservative 46; Mismatches 97; Indels 10; Gaps
4;

QY 1 MLWTWAVLPLVLAG-----SQLRVHTQGTNTSISLSIKLRRRHVHETDKNCSGLYQGGPFCC 56
Db 1 MGIWTLLPLVLTSVARLSKSSVNAQVTDINSKGLERKKTVTVTQNLQGLHHDGQFCH 60

QY 57 QPCQGGKKYEDCKWNGSTPTCACTEGEKYMDKNHYADKRCRCTLCDDEHGLEVEINCT 116
Db 61 KPCPPGKERKARDCHVNGDEPPCVPCQEGEKYTDKAHSSKRCRCRLCDDEHGLEVEINCT 120

QY 117 LTQNTKCKCPDFDYCDSPGCEHCVRCAACEHGTLEPCTATNTNCRKQSPRNLRLTLL 176
Db 121 RTQNTKCRCKPNFFCNSTVCSCHCDPCTKCEHGIKECTLTSNTKCKEGSRNLGLWCLL 180

QY 177 VLLPLV-VFYIRYKRKKCWKRRODDP--HSRTSSRETIPMNASNLISLKYIPRAEDM 232
Db 181 LLPLIIVWRKEVQKTRCKHRNENGSHSEPTLNPTVAINUSDVLSITTIYAGVM 240

QY 233 TIQBAKK--FARENNIKEGKIDEIMHDSIQDTABQKVQLLL 271
Db 241 TLSQVKANLCTLASKIOTIILKDLTSDSSENFNRNETOSLV 281

```

RESULT 15
US-10-041-574-3
; Sequence 3, Application US/10041574
; Patent No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian

APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-10-041-574-3

Query Match 35.8%; Score 645; DB 9; Length 281;
Best Local Similarity 45.6%; Pred. No. 5.8e-40;
Matches 128; Conservative 46; Mismatches 97; Indels 10; Gaps 4;
QY 1 MLTIWVLPVLAG----SQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYOGGPCC 56
DB 1 MGITWTLPLVLTSLVARLSSKSVNAQYTDINSKGLERKVTVTETONLEGLHHDGQFCH 60
QY 57 QPCOPGKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYNCT 116
DB 61 KPCPPGERKARDCTVNGDEPCVCEQKEYTDKAHFSKRCRCRLCDDEHGLEVEYNCT 120
QY 117 LTQNTKCKPDPYCDSPGCEHCVCASCCEHGTLEPCETATNTNCRKQSPNRNLWLTIL 176
DB 121 RTQNTKCRKPNFCNSTVCEHCDPCTKCEHIIKECTLTSTNCKKEGSRNLGLCLL 180
QY 177 VLLIPL-VFYRYKRYKRWKRRQDDP---ESRTSSRETIPMMNASNLSLSKYIPRIADM 232
DB 181 LLPIPLIVWVRKEVQKTRKHKENOGSHESPTLNPETVAINLSVDVLSKYITTTAGVM 240
QY 233 TIOEAKK--FARENNIKEGIDEIMHDSIODTAEQVQLLL 271
DB 241 TISQVKANLCTLAETIQTIIKDKITSDSENSFRNEIQSLV 281

Search completed: May 9, 2003, 17:09:17
Job time : 26.3006 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:02:31 ; Search time 28.1556 Seconds
(without alignments)
1116.509 Million cell updates/sec

Title: US-09-446-634A-23
Perfect score: 1804
Sequence: 1 MLWIWAVLPVLVLAGSQLRVH.....KDLGRKSTPTDGNENEGQCLE 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	A46484	apoptosis-mediati
2	1058.5	58.7	324	JC2395	Fas antigen precu
3	856	47.5	335	A40036	apoptosis-mediati
4	810.5	44.9	314	I37383	FAS soluble protei
5	305.5	16.9	149	S58662	Fas-Delta-(4,7) pr
6	203.5	11.3	271	S12783	Ox40 antigen precu
7	202	11.2	272	I48700	gene ox40 protein
8	194.5	10.8	277	A60771	B-cell activation
9	189.5	10.5	455	1 GQHUT1	tumor necrosis fac
10	185	10.3	454	1 GQHUT1	tumor necrosis fac
11	183	10.1	260	1 A46517	CD27 antigen precu
12	179.5	10.0	435	2 I54182	tumor necrosis fac
13	179	9.9	461	1 GQRTT1	tumor necrosis fac
14	171	9.5	277	2 I37552	Ox40 homolog - hum
15	169	9.4	461	2 JC4302	tumor necrosis fac
16	167	9.3	250	1 A49053	CD27 antigen precu
17	165.5	9.2	416	1 JN0006	nerve growth facto
18	165	9.1	305	2 A46476	B cell-associated
19	165	9.1	349	2 D72175	G2R protein - vari
20	163	9.0	348	2 T28623	hypothetical prote
21	163	9.0	349	2 D36858	gene G4R protein -
22	154.5	8.6	425	1 A26431	nerve growth facto
23	154.5	8.6	595	2 A42086	CD30 antigen precu
24	148	8.2	461	1 A35356	tumor necrosis fac
25	141	7.8	427	1 GQHUN	nerve growth facto
26	135.5	7.5	677	2 C42125	trophozoite cystei
27	126.5	7.0	1372	2 T25933	hypothetical prote
28	126	7.0	493	2 JC5486	membrane glycoprot
29	123.5	6.8	459	2 I48854	gene murine tumour

30	122.5	6.8	255	2	I38426	lymphocyte activat
31	122	6.8	103	2	I37384	FAS soluble protei
32	120.5	6.7	1111	2	T26972	hypothetical prote
33	119.5	6.6	474	2	B38634	tumor necrosis fac
34	119	6.6	2823	2	T23064	hypothetical prote
35	119	6.6	2823	2	F87908	protein T22A3.8 (1
36	119	6.6	3102	2	T43291	laminin alpha chai
37	116.5	6.5	325	2	B43692	T2 protein - rabbi
38	116	6.4	3712	2	S18253	laminin alpha-1 ch
39	115.5	6.4	1620	2	T27283	hypothetical prote
40	115.5	6.4	1816	1	S68960	laminin alpha-4 ch
41	115.5	6.4	3672	2	T23433	hypothetical prote
42	115.5	6.4	3704	2	T37316	probable laminin a
43	115	6.4	1274	2	T42017	cysteine rich prot
44	114	6.3	626	2	T04895	vacuolar sorting r
45	114	6.3	686	2	JC7569	Delta-4 protein -

ALIGNMENTS

RESULT 1

A46484
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenk
J. Immunol. 148, 1274-1279, 1992
A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas
A:Reference number: A46484; MUID:92148151; PMID:1371136
A:Accession: A46484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-327 <WAT>
A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A:Experimental source: BAM3 macrophage cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A:Title: Aberrant transcription caused by the insertion of an early transposable ele
A:Reference number: A47254; MUID:93189576; PMID:7680478
A:Accession: A47254
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Experimental source: MRL lpr/lpr
A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 100.0%; Score 1804; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 6.9e-122;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLWIWAVLPVLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPCCPCQ	60
DB	1	MLWIWAVLPVLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPCCPCQ	60
QY	61	PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCCTLCDEEHGLEVETNCTLTQN	120
DB	61	PGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCCTLCDEEHGLEVETNCTLTQN	120
QY	121	TKCKCKPDFYCDSPGCEHCVCASCEHGTLEPCPTATSNTRKOSPRNRLMLLTLVLLI	180
DB	121	TKCKCKPDFYCDSPGCEHCVCASCEHGTLEPCPTATSNTRKOSPRNRLMLLTLVLLI	180
QY	181	PLVFIYKRYKRRKCKWKRRQDDPESRTSSRETIPMNASNLSSKYPITRAEDMTTQEA	240
DB	181	PLVFIYKRYKRRKCKWKRRQDDPESRTSSRETIPMNASNLSSKYPITRAEDMTTQEA	240

QY 241 ARENNKEGKIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLIKGLKKAECRRITLD 300
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Db 241 ARENNKEGKIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLIKGLKKAECRRITLD 300
|||||
QY 301 KFQDMVQKDLGKSTPDGTGNNEGQCILE 327
|||||
Db 301 KFQDMVQKDLGKSTPDGTGNNEGQCILE 327
|||||
RESULT 2
JC2395
Fas antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: JC2395; PC2246
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A:Reference number: JC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395
A:Molecule type: mRNA
A:Residues: 1-324 <KIM>
A:Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487
A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, 'RFT' <K12>
A:Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A:Experimental source: liver
C:Genetics:
A:Introns: 62/1
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-324/Product: Fas antigen #status predicted <WAT>
F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NGF>
F:171-188/Domain: transmembrane #status predicted <TM>
Query Match 58.7%; Score 1058.5; DB 2; Length 324;
Best Local Similarity 61.1%; Pred. No. 1.5e-68;
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QY 1 MLMIWAVPLVLVLAGSOLRVHTQCTNSISLKLRRVHETDKNCSEGLYQGGPFCQPCQ '60
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Db 1 MLMIWAVPLVLVLAGSOLRVHTQCTNSISLKLRRVHETDKNCSEGLYQGGPFCQPCQ '60
|||||
QY 61 PGKKKVEDCKMNGGTPCTAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEFNTCTQN 120
|||||
Db 61 PGKRVKDCSTSGAPCTCHPTCEGEYTDKHYSDKRCRCAFCDEHGLEVEFNTCTQN 120
|||||
QY 121 TKCKKRPDPYCDSPGCEHCVRCASCE-HGTLEPCTATSNCRKQSPRNR-LWLLITLVL 178
|||||
Db 121 TKCRCKENYCNASLDCHGYCHTSCGLEDILEPCTRTNTCKKQSSNKLLWLLITLVL 180
|||||
QY 179 LPLVPLVYKRYKRCWKRRQDDPESRTSPRETIPMNASNLISKYIPRIAEADMTIQEAK 238
|||||
Db 181 ALVFIYKRYR-----KQPDGSGIPSPESVPMNVSDVNLNKYIWRTEAKMKICDAK 235
|||||
QY 239 KFARENNEKGEKIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLIKGLKKAECRRIT 298
|||||
Db 236 KEARQHKIPESKIDEHNSPDAAEQKQVOLLWCYQSHGSKSDAYODLIKGLKKAECRRIT 295
|||||
QY 299 LKFDQVQKDLGKSTPDGTGNNEGQCILE 327
|||||
Db 296 AEEIQAMWEDHENSISNRNENEGOSLE 324
|||||
RESULT 3
A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1

C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C:Accession: A40036; S24543; A38142
R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.;
Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can
A:Reference number: A40036; MUID:91309137; PMID:1713127
A:Accession: A40036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <ITO>
A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R:Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
A:Accession: S24543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <KRA>
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.;
J. Biol. Chem. 267, 10709-10715, 1992
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a mem-
A:Reference number: A38142; MUID:92268122; PMID:1375228
A:Accession: A38142
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-134, 'Q', 136-335 <OE>
A:Experimental source: SKW6.4 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)
A:Note: in NCBI backbone the source is designated as mouse
C:Genetics:
A:Gene: GDB:APT1
A:Cross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: NGF receptor repeat homology
C:Keywords: apoptosis; surface antigen; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:85-128/Domain: NGF receptor repeat homology <NG4>
F:174-190/Domain: transmembrane #status predicted <TM>
Query Match 47.5%; Score 856; DB 2; Length 335;
Best Local Similarity 49.4%; Pred. No. 4.8e-54;
Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;
QY 1 MLMIWAVPLVLVLAG-----SOLRVHTQCTNSISLKLRRVHETDKNCSEGLYQGGPFCQ 56
|||||
Db 1 MLGIWITLLPLVLTAVRLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
|||||
QY 57 QPCQPGKKKVEDCKMNGGTPCTAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEFNTCT 116
|||||
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDDEHGLEVEFNTCT 120
|||||
QY 117 LTQNTKCKKPPDYCDSPGCEHCVRCASCEHGTLEPCTATSNCRKQSPRNRLLWLLITLV 176
|||||
Db 121 RTQNTKCRCKPNFECNSTVCEHCDPCTCKEHLIKETCTLSNTCKCKEESRNLGLCLL 180
|||||
QY 177 VLLIPL-VFIYKRYKRCWKRRQDDP-----ESRTSSRETIPMNASNLISKYIPRIAEAD 232
|||||
Db 181 LPLIPLVWVKRKEVQKCTCRKHKNQSGHESPTLPNETVAIINLSDVLSKYITTTAGVM 240
|||||
QY 233 TTQEAFFKFARENNKEGKIDEIMHDSIQDTAEQKQVOLLWCYQSHGSKSDAYODLIKGLK 292
|||||
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVOLLRNWHLHGKKEAYDTLIKDLKK 300
|||||
QY 293 AECRRITLDRFQDMVQKDLGKSTPDGTGNNEGOCIL 326
|||||
Db 301 ANLCTLAEKIQTIIILKDTSDSENSENFRENIQSL 334
|||||
RESULT 4
I37383
FAS soluble protein - human

C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I37383
R:Casino, I.; Fuccel, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A:Reference number: I37383; MUID:95181785; PMID:7533181
A:Accession: I37383
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <RES>
A:Cross-references: EMBL:Z47993; NID:9728578; PIDN:CAA88031.1; PID:9695539

Query Match 44.98; Score 810.5; DB 2; Length 314;
Best Local Similarity 46.88; Pred. No. 8.1e-51;
Matches 156; Conservative 50; Mismatches 100; Indels 27; Gaps 3;

Qy 1 MLWNAVLPLVLG-----SQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPPCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERLKTVTVTETQNLEGLHHDGQFCH 60
Qy 57 QPCPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCLDDEHGLEVETNCT 116
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAAHFSSKRCRCLDDEHGLEVETNCT 120
Qy 117 LTQNTKCKRPFYCDSPGCEHCVRCAACEHGTLEPCTATNTNCRKSPRNRLMLTLIL 176
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNCKKEB----- 168
Qy 177 VLLPLVFIYKRYKRCWKRRQDDP-----ESRTSSRETIPNANSLSKYIPRIADMT 233
Db 169 -----VKRKEYQKTRKRKENQGSHEPTLPNPTVAINLSVDVLSKYITTIAGVMT 220
Qy 234 IQEAKPFARENKKEGKIDETMHDSDIOTAEQYQVLLICWYQSHGSKSDAYODLKLKKA 293
Db 221 LSQVKGKRVKNGVNEAKIDEKNDVQDTAEQYQVLLRNWHLQHGKREAYDTLKLKKA 280
Qy 294 ECRTLDKFDQMDVKDLGKSTPDPGNEGQCL 326
Db 281 NLCTLAETQIWLKIDTSDSENSFNREIQSL 313

RESULT 5
S58662
Fas-Delta-(4,7) protein - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 01-Dec-2000
C:Accession: S58662; S57566
R:Liu, C.; Cheng, J.; Mountz, J.D.
Biochem. J. 310, 957-963, 1995
A:Title: Differential expression of human Fas mRNA species upon peripheral blood mononuc
A:Reference number: S58662; MUID:96013198; PMID:7575433
A:Accession: S58662
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-149 <LIU>
R:Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57565
A:Accession: S57566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <SCH>
A:Cross-references: EMBL:X89101; NID:9887457; PID:9887458
C:Keywords: alternative splicing

Query Match 16.98; Score 305.5; DB 2; Length 149;
Best Local Similarity 42.99; Pred. No. 5.5e-15;
Matches 63; Conservative 20; Mismatches 47; Indels 17; Gaps 4;

Qy 1 MLWNAVLPLVLG-----SQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPPCC 56
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERLKTVTVTETQNLEGLHHDGQFCH 60

Qy 57 QPCPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCLDDEHGLEVET--- 113
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAAHFSSKRCRCLDDEHGVNNESSRN 120
Qy 114 -NCTLTQNTKCKRCPD-----FYC 131
Db 121 AHSPTATPSAKRK-DPDLTWGGFVFPFC 146

RESULT 6
SL2783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: SL2783; S08036
R:Mallett, S.; FCSum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lympho
A:Reference number: SL2783; MUID:90214614; PMID:2157591
A:Accession: SL2783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-27/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 11.38; Score 203.5; DB 2; Length 271;
Best Local Similarity 24.48; Pred. No. 1.9e-07;
Matches 64; Conservative 27; Mismatches 82; Indels 89; Gaps 11;

Qy 2 LWNVAVLP--LVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYGGPPCCQPC 59
Db 1 MYVWVQPTAFLLGLSLGV-----TVKL-----NCVKDTPSGHKCCRC 41
Qy 60 QPGKKKVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRCLDDEHGLEVETNCTLTO 119
Db 42 QPGHGMVSRCDHTRDT-VCHPCEPG-FYNEAVNY-DTCQCTQCNRHSGSELUKQCTPTE 98
Qy 120 NTKCKCKPDFY-----CD-----SPG-----CEHCVRCAACEHGTLEPCTAT 156
Db 99 DTVCQCEGTQPRODSSHKLGVDCVPCPPGHPSPGNSQACKPWTNCTLSGKQIRHPASNS 158
Qy 157 SNTNCRKOS-----PRNRLMLTI----- 175
Db 159 LDTVCEDRSLLATLLWETQRTTFRPTTVPSTTVPRTSQLPSTPTLVAPGPAFAVILGL 218
Qy 176 -LVLLIPLVFIYKRYKRCWK 196
Db 219 GLGLIAPLTVLLALYLLRKAWR 240

RESULT 7
I48700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.N.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:9312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.

Eur. J. Immunol. 25, 926-930, 1995
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
 A:Reference number: I48334; MUID:95255413; PMID:773295
 A:Accession: I48334
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-14,'G',16-272 <RE2>
 A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
 C:Genetics:
 A:Gene: ox40
 A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 11.2%; Score 202; DB 2; Length 272;
 Best Local Similarity 26.5%; Pred. No. 2.5e-07;
 Matches 69; Conservative 22; Mismatches 85; Indels 84; Gaps 12;

OY 2 LWMVAVPLVLGASOLRVHTGNTSISLSKLRVHETDKNCSGLYGGPFCCQPCQP 61
 DB 1 MIVVWQQPTALL---LLALTILGVA-----RRLL-----NCVKHTYPSGHKCCRECQP 44
 OY 62 GKKKVEDCKMNGGPTCAPCTEGKEYMDKNHYADKRCCTLCDEHGLEVTNCTLTQNT 121
 DB 45 GHGMYSRCDHRTDT-LCHPCETG-FYNEAVNY-DTCQKCTQCNHRSGSELKQNCPTQDT 101
 OY 122 KCKKPDY-----CD-----SPG-----CEHCVRC----- 142
 DB 102 VCRCPGTQPRQDSYKLGVDVCPGPFHFGNNAQKPTWNTLSGKQTRHPASDLD 161
 OY 143 ASCE-----HGILEPCTATSNCRKQS-----PNRNLWLLTIL 176
 DB 162 AVCEDSLATLWETQRTFRPTTVQSTVWPTSELSPPTLVTPEGPAFALLGLGL 221
 OY 177 VLLIPLVFIYKRYKRWCK 196
 DB 222 GLLAPLVLLALYLLRAWR 241

RESULT 8
 A60771
 B-cell activation protein CD40 precursor - human
 N:Alternate names: B-cell surface antigen Bp50
 C:Species: Homo sapiens (man)
 C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S04460; A60771
 R:Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBO J. 8, 1403-1410, 1989
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A:Reference number: S04460; MUID:89356608; PMID:2475341
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <STA>
 A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
 R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
 A:Reference number: A60771; MUID:89093941; PMID:2463309
 A:Accession: A60771
 A:Molecule type: protein
 A:Residues: 21-50 <BRA>
 A:Experimental source: Burkitt lymphoma cell line Raji
 C:Genetics:
 A:Gene: GDB:CD40
 A:Cross-references: GDB:215268; OMIM:109535
 A:Map position: 20q12-20q13.2
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:2194-2195/Domain: extracellular #status predicted <EXT>
 F:194-2195/Domain: transmembrane #status predicted <TM>
 F:216-277/Domain: intracellular #status predicted <CYT>
 F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.8%; Score 194.5; DB 2; Length 277;
 Best Local Similarity 28.6%; Pred. No. 8.6e-07;
 Matches 59; Conservative 20; Mismatches 74; Indels 53; Gaps 8;

OY 37 VH-ETDKNCSGLYGGPFCCQPCQPGKRRKVEDCKMNGGTPPTCAPCTEGKEYMDKNHYAD 95
 DB 18 VHPPTTACREKQYLINSQCCLQPGQKLVSDCTFEFTET-ECLPCGE-SEFLDTWNRRT 75
 OY 96 KCRCTLCDEHGLEVTNCTLTQNTKCKKPDYCDSPGCHVCVRCASCEHG----- 148
 DB 76 HCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACSCVLHRSCLSPGFGVKQIA 135
 OY 149 -----TLEPCTA--TSN-----TNCRKO----- 173
 DB 136 TGVSDTICEPCVPGVFFSNVSAFCKCHPTWCETKDLVQQAGTNKTDVCGCPDRLRAL 195
 OY 174 TIL-----VLLIPLVFIYKRYK 191
 DB 196 VVIPIFGILFAILLVLVFIKRVAK 221

RESULT 9

GQUT1

tumor necrosis factor receptor 1 precursor [validated] - human
 N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
 C:Accession: A38208; A34899; A34900; A36555; A38281; S12057; JT0758; A60231;
 R:Fuchs, P.; Striehl, S.; Dworzak, M.; Hummler, A.; Ambros, P.F.
 Genomics 13, 219-224, 1992
 A:Title: Structure of the human TNF receptor 1 (p50) gene (TNRF1) and localization t
 A:Reference number: A38208; MUID:92250049; PMID:131517
 A:Accession: A38208
 A:Molecule type: DNA
 A:Residues: 1-455 <FUC>
 A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; P
 R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Les
 Cell 61, 351-359, 1990
 A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor r
 A:Reference number: A34899; MUID:90235284; PMID:2158862
 A:Accession: A34899
 A:Molecule type: mRNA
 A:Residues: 1-455 <LOE>
 A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
 A:Experimental source: placenta
 A>Note: part of this sequence, including the amino end of the mature protein, confir
 R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
 Cell 61, 361-370, 1990
 A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fac
 A:Reference number: A34900; MUID:90235285; PMID:2158863
 A:Accession: A34900
 A:Molecule type: mRNA
 A:Residues: 1-455 <SCH>
 A:Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
 R:Hummler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
 DNA Cell Biol. 9, 705-715, 1990
 A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
 A:Reference number: A36555; MUID:91090841; PMID:1702293
 A:Accession: A36555
 A:Molecule type: mRNA
 A:Residues: 1-455 <HIM>
 A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
 A:Accession: C36555
 A:Molecule type: protein
 A:Residues: 30-38; 41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104; 107-128; 162-167, 'X', 16
 A>Note: the purified protein, called tumor necrosis factor binding protein, is a solu
 R:Gray, P.W.; Barrett, K.; Chantray, D.; Turner, M.; Feldmann, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
 A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
 A:Reference number: A38281; MUID:91017509; PMID:2170974
 A:Accession: A38281

A;Molecule type: mRNA
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 and TGG for residue 373.
R;Nophr Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
A;Accession: S12057
A;Molecule type: mRNA
A;Residues: 1-455 <KEM>
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A;Note: Parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were cloned from a cDNA library.
R;Kemper, O.; Wallach, D. Gene 134, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor receptor.
A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <KEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M. Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence, and characterization of an inhibitor (soluble tumor necrosis factor inhibitor).
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le Proc Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor inhibitor).
A;Reference number: A38258; MUID:91062364; PMID:2174164
A;Accession: A38258
A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G. Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from human urine.
A;Reference number: A60594; MUID:89171156; PMID:2924890
A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43, 'X', 45-53, 'Y', 55-57, 'XK', 60 <OLS>
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct murine tumor necrosis factor receptors.
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-45 <ENG>
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kirihaara, S.; Kato, K. Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
A;Reference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAG>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
C;Genetics:
A;Gene: GDB:125913; OMIM:191190
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
C;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type I; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-45/Domain: signal sequence #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted

F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane status predicted <MEM>
F;235-455/Domain: intracellular status predicted <INT>
F;54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted
Best Match 10.5%; Score 189.5; DB 1; Length 455;
Best Local Similarity 24.7%; Pred. No. 3; le-06;
Matches 67; Conservative 31; Mismatches 112; Indels 61; Gaps 11;
QY 7 VLPVLVAGSOLRVHTQGTNISSESLKLRVRVHETDKNCSEGLY---OGGPFCCQPCQPGK 63
Db 10 LLPVLLELLVGVIPSGVIGLVPHLGDREK---RDSVCPQGYIHPQNNSTCCCTCKHGT 66
QY 64 KKVEDCKKNGTPTCAPCTGEGKYMKNHVDKCRRTCLDEBHGLEVETNCTLTONTKC 123
Db 67 YLYNDCRPGQDPTDCRECSGSFTASENHLLR-HCLSCSKRKEMGQVEISSCTVDRTVC 125
QY 124 KCRPDFYCD--SPGCEHCVRCAECHEGTLT-PCATATNT-----NCC 161
Db 126 GCRKNQRYHWSENLFCFNCISLNGTIVHLSQCEKQNTVCTCHAGFFLRENECVCSNC 185
QY 162 RKQSPRNLWL-----LTIL-----VLLPLVFIYKRYKRCWK---- 196
Db 186 KKSLECKKLCPLQETENYKGTEDSGTTLVPLVIFVGLLCLLFLGLMYRQYR-WKSKLY 244
QY 197 -----RRQDDPESNTSSRTIPMNASLSLS 222
Db 245 SIYCGKSTPEKEGELETTTKPL-APNPSFS 274
RESULT 10
QOMST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I34532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors.
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors.
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fe Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.
A;Reference number: S16677; MUID:91285014; PMID:1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R;Rothe, J.G.; Brückhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID:92039815; PMID:1657766
A;Accession: S19021
A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R;Bebo, B.F.

A:Molecule type: mRNA
A:Residues: 1-58, 'A', 60-260 <CAM>
A:Cross-references: GB:M63928; NID:G180084; PIDN:AAA58411.1; PID:G180085
A:Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBI:P:60289)
C:Comment: A soluble CD27 found in serum and urine is formed by proteolysis.
C:Genetics:
A:Gene: GDB:CD27
A:Cross-references: GDB:I32582; OMIM:186711
A:Map position: 12p13-12p13
A:Introns: 46/1; 90/1; 150/1; 180/1; 220/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-260/Product: CD27 antigen #status predicted <MAT>
F:21-191/Domain: extracellular #status predicted <EXT>
F:27-63/Domain: NGF receptor repeat homology <NG>
F:65-105/Domain: NGF receptor repeat homology <NG>
F:121-188/Region: proline/serine/threonine-rich
F:192-211/Domain: transmembrane #status predicted <TMN>
F:212-260/Domain: intracellular #status predicted <INT>
F:95/Binding site: carbohydrate (Asn) #status predicted

Query Match 10.1%; Score 183; DB 1; Length 260;
Best Local Similarity 36.4%; Pred. No. 5.4e-06;
Matches 36; Conservative 11; Mismatches 48; Indels 4; Gaps 3;

QY 42 KNCSEGLYOG-GPFCQCPQPKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRC 100
Db 25 KSPERHYAQQKLCQCEPGTFLVKDCQDHRKTAQCDPCIPGVSPDHHTRPHCESC 84
QY 101 TLCDEHGLEVTNCTLTONTCKKPKDPYCDSPGCEHC 139
Db 85 RHCONS--GLLVR-NCTITANAEACRNGWQCRDKECTEC 120

RESULT 12
I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a cDNA library of human 12p transcribed se-
A:Reference number: I54182; MUID:93252381; PMID:8486360
A:Accession: I54182
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; NID:G339761; PIDN:AAA36757.1; PID:G339762
C:Genetics:
A:Gene: GDB:L7BR
A:Cross-references: GDB:I230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 10.0%; Score 179.5; DB 2; Length 435;
Best Local Similarity 25.5%; Pred. No. 1.5e-05;
Matches 65; Conservative 27; Mismatches 98; Indels 65; Gaps 12;

QY 1 MLWTWAVL-----PLVLAGSQLRVHTQGTNNTSISLKLRRRVHETDKNCSEGLYOGGP 53
Db 1 MLPLWATSAPGLAWPLVLGLFGLLAASQ-PQAVPPYASENQTCDQKEYEYEPQHR--- 56
QY 54 FCQCPQPKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEHGLEVET 113
Db 57 ICCRCPPPGTYSAKCSRIRDY-VCATCAE-NSYNHWNLTLCQLCRCPDPMVGLLEIA 114
QY 114 NCTLTONTCKKPKDPYCDOS-----PGCE-----HCVRCA-- 144
Db 115 PCTSKRTQCRQPGMFCFAAWALECTHCELLSDCPGTEALKDEVGKGNHCVCPKAGH 174
QY 145 -----CEH-GTLE--PCTATSNTCR----KOSPRNRLWLLTILVLLIPL 182

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OY 1 MLMIAVPLVLAGSOLRVHTOGTNSISLSKLRHREHETDKNCSGLYOGPFCCOPQ 60
 Db 1 MGIWVLLPIL-----TCLASLSLSTSIINDCKIKNETGYSTG---YLSGNFCOLCP 49
 OY 61 PGKKVYEDCKMNGGTPFCAPCTEGKEYMDKNHYADKCRCTLCDDEHGLEVEINCLTQN 120
 Db 50 PGTKKADCTSNNGKPCDCEGGEYTDKSHFSSKCRCLDGBHGLEVEITDCTTQN 109
 OY 121 TKCKPDPFYCDSPGCEHCVRASCSEHGTLEPCTATSNCRKO-----SPRNRMLLTI 175
 Db 110 TKRCKSNFNCALKECHDPCITMCEHGLEIECTQTSNCKCKSGSTGSKHFFMLTCT 169
 OY 176 LVLLIPLVFYTKRYKRRKCKKRRROD 200
 Db 170 L-LIIPVLGLRRYKHKHOGKHGYD 193

RESULT 14
 O9DGH8 PRELIMINARY; PRT; 312 AA.
 AC O9DGH8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Fas antigen (Fragment).
 GN FAS.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bridgman J.T., Johnson A.L.;
 RT "Fas Expression and Regulation in Hen Granulosa Cells."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF296874; AAC02242.1; -
 DR HSSP; O14763; ID4V.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF000531; death; 1.
 DR Pfam; PF00020; TNFR_C6; 2.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 312 AA; 35275 MW; 5496BCF1E4CE676C CRC64;

Query Match 24.3%; Score 438; DB 13; Length 312;
 Best Local Similarity 35.1%; Pred. No. 6.8e-31;
 Matches 91; Conservative 46; Mismatches 108; Indels 14; Gaps 5;

OY 55 CCOPQCGKKKVEDECKMNGGTPFCAPCTEGKEYMDKNHYADKCRCTLCDDEHGLEVEIN 114
 Db 6 CCTKCKRGHVKSIDCPRT--QAHCVPRKSGEYIMDHINDLDECMKRCSCKALGLEEVKN 63
 OY 115 CTLTONTKCKKPDYCDSPGCEHCVRASCSEHGTLE-PCATATSNCRKOSPNNRLMLL 173
 Db 64 CTSTENACSCAKNHYNSSRCEHCECTVCENGQIEKECTSTSDYVCRMGACMPWGT 123
 OY 174 TLVLLI-----PLVFTYKRYKRRKCKKRRDDPESTRS---SRETIPMANSLSLSKY 224
 Db 124 ALIVFVILAAVAGLIIFYEK--RKVNNYTTQGTAAADTKVHSPETLRLIHIDVLTTH 181
 OY 225 IPIAEDMTIOAKKFARENNIKEGKIDELMHDSIODTAOKVOLLCWYQSHGKSDAYQ 284
 Db 182 VEDIYRENTLEQMTFVRHRLSEPTIYETLIDNKNNTSEOKIKLFQKWKYQKHGGAIVE 241
 OY 285 DLIKGKRAECRRITLDFQ 303

Db 242 TLICSLIDLKMRTADKIE 260

RESULT 15
 O9DGH7 PRELIMINARY; PRT; 285 AA.
 AC O9DGH7;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Fas ligand receptor soluble form (Fragment).
 GN Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bridgman J.T., Johnson A.L.;
 RT "Fas Expression and Regulation in Hen Granulosa Cells."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF296875; AAC02243.1; -
 DR HSSP; O14763; ID4V.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF000531; death; 1.
 DR Pfam; PF00020; TNFR_C6; 2.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 285 AA; 32431 MW; A9761960CCD79F6D CRC64;

Query Match 23.8%; Score 428.5; DB 13; Length 285;
 Best Local Similarity 34.4%; Pred. No. 4.3e-30;
 Matches 86; Conservative 39; Mismatches 102; Indels 23; Gaps 3;

OY 55 CCOPQCGKKKVEDECKMNGGTPFCAPCTEGKEYMDKNHYADKCRCTLCDDEHGLEVEIN 114
 Db 6 CCTKCKRGHVKSIDCPRT--QEHCVPCKGEYIMDHINDLDECMKRCSCKALGLEEVKN 63
 OY 115 CTLTONTKCKKPDYCDSPGCEHCVRASCSEHGTLE-PCATATSNCRKOSPNNRLMLL 173
 Db 64 CTSTENACSCAKNHYNSSRCEHCECTVCENGQIEKECTSTSDYVCRMGACMPWGT 114
 OY 174 TLVLLIPLVFTYKRYKRRKCKKRRDDPESTRSSRETIPMANSLSLSKYIPIAEDMT 233
 Db 115 -----VKRRVNNYTTQGTAAADTKVHSPETLRLIHIDVLTTHHVDIVREMT 163
 OY 234 IQEAKFARENNIKEGKIDELMHDSIODTAOKVOLLCWYQSHGKSDAYODLTKGLKA 293
 Db 164 LEQVTFVRHRLSEPTIYETLIDNKNNTSEOKIKLFQKWKYQKHGGAIVETLCSLRL 223
 OY 294 ECRRTLDFQ 303
 Db 224 KMRTAADKIE 233

Search completed: May 9, 2003, 17:06:48
 Job time : 29.6495 secs


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Db 238 ITEVEFVRKNGEAKIDIDHNDLHETAQKVOLLRWYQSHGKNAYCTLTNLPRK 297
QY 294 ECRRLDKFQDMQVKDLGKSTPDTGNENEGQCL 326
Db 298 ----LAEKICDVLKIDITNERENANLQNESEN 326

RESULT 11
Q9GK28 ID Q9GK28 PRELIMINARY; PRT; 310 AA.
AC Q9GK28;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fas antigen APO-1/CD95.
CN FAS.
OS Macaca arctoides (Stump-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9540;
RN [1]
RP SEQUENCE FROM N.A.
RA Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;
RT "Cloning of fas gene in stump-tailed monkey.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332357; AG49394.1; -.
DR HSSP; P25445; IODF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 310 AA; 34806 MW; C5C79BF1F804A419 CRC64;

Query Match 42.6%; Score 768; DB 6; Length 310;
Best Local Similarity 47.6%; Pred. No. 3.2e-60;
Matches 156; Conservative 41; Mismatches 101; Indels 30; Gaps 6;

QY 1 MLWIAVPLVLAGSOLR-----VHTQGISISESLKRRVHETDKNCSEGLYQGPF 55
Db 1 MLCWTLLPLVLT-SVRLLSKCVNAQVTDISSKGFELRKIVTTIETQNLGLHGGQFC 59
QY 56 CQCPQKXKVEDCKMNGGTPTCAPTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEY 115
Db 60 RNPCCPGERKARDCTVNEDEPDCVPCQEGKEYTDKGFSSKRCRCLCDDEHGLEVEY 119
QY 116 TLQNTKCKKPDFYCDSPGCEHVCASCSEHGTLPCTATSNTRKQSPRNLWLLTI 175
Db 120 TRQNTKCKKPNFFCNVSAVCEHCDPCTCKHGIIECTLTNTKCKE----- 168
QY 176 LVLLIPLVFIYKRYKRCWKRRQDDPESRTSSRETIPNANSLSKYIPRIADMTIQ 235
Db 169 -----VVIKPCRKHR--KENQGPHESTTLNPET-AINLSDVDLSKYITTIAGAMT 218
QY 236 EAKKFARENNIKEGKIDIMHDSIQDARQKVOLLWCWQSHGKSDAYODLLKGLKARC 295
Db 219 QVKDFVRKNGVSEAKIDEIKNNHVQDARQKVOLLRWYQLHGGKADCTLLKGLKTADL 278
QY 296 RTILQKFDQWQKDLGKSTPDTGNENEG 323
Db 279 CTLAEKIHAVILKDI---TSDTENSNGF 303

RESULT 12
Q9R230 ID Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;

Query Match 28.9%; Score 520.5; DB 6; Length 263;
Best Local Similarity 48.8%; Pred. No. 2.6e-38;
Matches 100; Conservative 27; Mismatches 61; Indels 17; Gaps 4;
```

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=CORPUS LUTEBUM;
RA Lareu R.R., Dharmarajan A.;
RT "Cloning and expression of Fas and Fas Ligand in the apoptotic rat
corpus luteum.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD20221.1; -.
DR HSSP; P25942; LCDP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 33.8%; Score 609.5; DB 11; Length 150;
Best Local Similarity 69.3%; Pred. No. 1.7e-46;
Matches 104; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

QY 6 AVLPVLVLAGSOLRVHTQGISISESLKRRVHETDKNCSEGLYQGPFCCQCPQK 65
Db 1 AVLPVLVLAGSOLRVHTQGISISESLKRRVHETDKNCSEGLYQGPFCCQCPQK 60
QY 66 VEDCKMNGGTPTCAPTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYNTLTQNTKCK 125
Db 61 VKDCTTSGAPTCHPCTEGEYTDKHYSDKRCRCACDEGHGLEVEYNTLTQNTKCK 120
QY 126 KPQFYCDSPGCEHVCASCSE-HGTLEPCT 154
Db 121 KENFYCNASLDCYHCTSCGLEIDLEPCT 150

RESULT 13
Q9XS60 ID Q9XS60 PRELIMINARY; PRT; 263 AA.
AC Q9XS60;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fas antigen spliced variant.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021297; BAA78429.1; -.
DR HSSP; O14763; 1DAV.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 263 AA; 30374 MW; 6D76782ADEDBFD7 CRC64;

Query Match 28.9%; Score 520.5; DB 6; Length 263;
Best Local Similarity 48.8%; Pred. No. 2.6e-38;
Matches 100; Conservative 27; Mismatches 61; Indels 17; Gaps 4;
```

Db	60	RNCPGPERKARDCTVNEDEPCVPCQEGKEYTDKGHLSSKRRRCRLCDEGHGLEVEINC	119
Qy	116	TLTQNTKCKCKPDFYCDSPGCEHCVCACSEHGTTLEPCTATSTWNCRKQSPNRLL-WLLT	174
Db	120	TRTQNTKCKCKPDFYCDSPGCEHCVCACSEHGTTLEPCTATSTWNCRKQSPNRLL-WLLT	179
Qy	175	ILVLLPLVFIYKRYKRWKRRDDPSRTSSRETTPMNASNLSLSKIYIPRIAEADMTI	234
Db	180	LLLLIPVIVVVIKKACRKHRENQPHSTTLNPET-AINLSDVLSKYITTAGATWL	238
Qy	235	QEAKKFARENKIEKGIEMHDSIQDTAEQVOLLWCYQSHGSKSDAYQDILIKGLKAE	294
Db	239	SOVKDFYKRGVSEAKIDEIKNDVQDTAEQVQLPNNYQLHGKKDCACTLIKGLKTAD	298
Qy	295	CRRTLDKFQDMVKDLGKSTPTDGTGNEG	323
Db	299	LCTLAEKIHAIVILKDI---TSDTSENSNFG	324
RESULT 10			
O97491	ID	PRELIMINARY;	PRT; 327 AA.
AC	097491;		
DT	01-MAY-1999	(TReMBLrel. 10, Created)	
DT	01-MAY-1999	(TReMBLrel. 10, Last sequence update)	
DT	01-JUN-2001	(TReMBLrel. 17, Last annotation update)	
DE	Fas protein.		
GN	FAS.		
OS	Fas arises (Sheep).		
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIMPHOCYTE;		
RA	Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;		
RT	"Cloning of sheep fas antigen.;"		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB011671; BAA37093.1; -		
DR	HSSP; P25445; 1DDF.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR001368; TNFR_c6.		
DR	Pfam; PF00531; death; 1.		
DR	Pfam; PF00020; TNFR_c6; 3.		
DR	SMART; SM00005; DEATH; 1.		
DR	SMART; SM00208; TNFR; 3.		
DR	PROSITE; PS00017; DEATH DOMAIN; 1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.		
DR	PROSITE; PS00500; TNFR_NGFR_2; 2.		
SQ	SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;		
Query Match 44.5%; Score 802; DB 6; Length 327;			
Best Local Similarity 47.7%; Pred. No. 3.2e-63;			
Matches 159; Conservative 48; Mismatches 112; Indels 14; Gaps			
Qy	1	MWIIWAVLPVLVLAGSQL-----RVHTQGTNSISLKLRRRVHETDKNCSGLYGGPFF	54
Db	1	MSGIWHLSLPIFISVSRPLSKGENAHVAGIN--SEGURLNKNITGA--SSQEGLYREHLF	57
Qy	55	CCQCPQPKKKVEDCKMNGGTTCPACTEGREYMDKNHYADKCRRCRLCDEEHLGVETN	114
Db	58	CCQCPPPGKRKNGCDCKRDGMPCEVCVLCSEGNEYTDKSHHSDKIRCSVCDEEHLGVETN	117
Qy	115	CHLTQNTKCKCKPDFYCDSPGCEHCVCACSEHGTTLEPCTATSTWNCR-KOSPNNRLWLL	173
Db	118	CHTQNTKCRCKSNFPCNSPCEHCNPTTCEHGLIEKCTPTSTKCKGSRHTNSLWAL	177
Qy	174	TILVLLPLVFIYKRYKRWKRRDDPSRTSSRETTPMNASNLSLSKIYIPRIAEADMT	233
Db	178	LILLLILILFLIYKVRRRRNKNGVCSAASDEGRQLNLTVDVLGKYPISIAELMK	237
Qy	234	IQEAKFARENKIEKGIEMHDSIQDTAEQVOLLWCYQSHGSKSDAYQDILIKGLKKA	293

RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021298; BAA78430.1; -;
DR HSSP; P25445; 1DDF
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

Query Match 45.5%; Score 820; DB 6; Length 319;
Best Local Similarity 49.4%; Pred. No. 7.8e-65;
Matches 166; Conservative 44; Mismatches 98; Indels 28; Gaps 7;

QY 1 MLWIAVLPLVLGASQRLVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQ 60
Db 1 MTGIWVLLPLIL-----TCIASLSTINDCKIKNETQYSTG---YLSGNFCCQLCP 49
QY 61 PGKKVDECKNGGTPTCAPTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYETCTLTQN 120
Db 50 PGTKKADCTNECKPDCEPCQEGEYDYSKSHFSSKRCRCLCDDEHGLEVEYETCTLTQN 109
QY 121 TKCKCKPFCYDSCPCGEHVCASCHECTLEPCATSTNCRKQ-----SPNRRLWLT 175
Db 110 TKCKCKNFFCNALKECHDCPTCEHGIIEECTQTSNCKRGSTTGGKHLFWLSTL 169
QY 176 LVLLIPLVFIYKRYKRCWKRRQDDPSRTSSRETIPMNASLNSLSKYIPRIADMTIQ 235
Db 170 --LLIPIVLGRYKRYKRGKGYD--KSTALIEGVPFMFSDVDISKYIPTIAEEMKIN 225
QY 236 EAKKFARENNIKGKIDEMHDSIQDTAEQVQLLLCYQSHGSKSDAYQDLIKGLKAE 295
Db 226 EYEFVRKNGVNEAKIDEIKNDNIQDTAEQVQLLRNWHOLRGKDAYNTLIKGLRANTL 285
QY 296 RRTLDKFDQVQKDLGKSTPDGTG-----ENEGCL 326
Db 286 CALAEKIQDIVQKDI---TSDHNDLIRDEKERQSL 318

RESULT 7
QYBDN4
ID QYBDN4 PRELIMINARY; PRT; 331 AA.
AC QYBDN4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fas antigen CD95.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Cercopithecinae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344843; AAK37602.1; -;
DR HSSP; P25445; 1DDF
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 R -> Q.
FT VARIANT 55 55 E -> Q.
FT VARIANT 60 60 R -> H.
FT VARIANT 61 61 N -> S.
FT VARIANT 77 77 E -> G.
FT VARIANT 95 95 E -> A.
FT VARIANT 282 282 E -> G.
FT VARIANT 298 298 E -> D.
FT VARIANT 300 300 C -> *.
SQ SEQUENCE 331 AA; 37277 MW; 1D843C4DEID343F4 CRC64;

Query Match 45.3%; Score 816.5; DB 6; Length 331;
Best Local Similarity 49.5%; Pred. No. 1.7e-64;
Matches 163; Conservative 46; Mismatches 109; Indels 11; Gaps 5;

QY 1 MLWIAVLPLVLGASQRLVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCC 55
Db 1 MGIWVLLPLVLVT-SVRLLSKCVNAQVTDINSKGFELRKIVTTIETRNLEGLHHEGQFC 59
QY 56 COPCOPGKKKVEDCKMNGGTPTCAPTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYETNC 115
Db 60 RNPCCPGGERKARDCTVNEDEPCVPCQSGKEYTDKGHSSKRCRCLCDDEHGLEVEYETNC 119
QY 116 TLTONTRCKCKPFCYDSCPCGEHVCASCHECTLEPCATSTNCRKQSPR-NRLWLT 174
Db 120 TRTONTKCRKPNFPCNSAVCEHGDPCPTCKKHGIIIEECTLTSTNCKEEDSRSDLLWLCL 179
QY 175 ILVLLIPLVFIYKRYKRCWKRRQDDPSRTSSRETIPMNASLNSLSKYIPRIADMTI 234
Db 180 LLLIPIVYVVIKACRKHRENQGHSTETLNPET-AINLSDVDSLKYITTAGGTL 238
QY 235 QEAKKFARENNIKGKIDEMHDSIQDTAEQVQLLLCYQSHGSKSDAYQDLIKGLKAE 294
Db 239 SQVRDFYKNGVSEAKIDEIKNDNIQDTAEQVQLLRNWHOLRGKDAYNTLIKGLTAG 298
QY 295 CRRTLDKFDQVQKDLGKSTPDGTGNEFG 323
Db 299 LCTLAEKIHAVILKDI---TSDTENSFNFG 324

RESULT 8
QYGL40
ID QYGL40 PRELIMINARY; PRT; 334 AA.
AC QYGL40;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fas antigen.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Cercopithecinae;
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Shui B., Chi L., Zhang Y.R.;
RT "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007572; AAG16762.1; -;
DR HSSP; P25445; 1DDF
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.

```
RESULT 4
Q9BDN0 Q9BDN0 PRELIMINARY; PRT; 331 AA.
AC Q9BDN0
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE FAS antigen CD95.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -.
DR HSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR VARIANT 75 75 V->A.
FT VARIANT 89 89 E->K.
FT VARIANT 196 196 E->K.
FT VARIANT 201 201 R->H.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 45.8%; Score 825.5; DB 6; Length 331;
Best Local Similarity 49.8%; Pred. No. 2.7e-65;
Matches 164; Conservative 46; Mismatches 108; Indels 11; Gaps 5;

QY 1 MLWTWAVPLVLAGSQLR-----VHTQGTNSISLSKLRRVHETDKNCSGLYOGGPGFC 55
DB 1 MLGIWTLPLVLT-YVRLLSKCVNAQVTDISSKGFELRKIVTTIETQNLGLHHEGQFC 59
QY 56 CQCPQCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCLDDEHGLEVEYTC 115
DB 60 RNPCCPGERKARDCTVNEDEPDCVPCQEGEYTDKGHFSKRCRLCDEGHGLEVEINC 119
QY 116 TLQNTCKCKPDYCDSPGCEHCVCASCHEGTLEPCTATSNTRKQSPRNL-WLLT 174
DB 120 TRQNTCKCRKPNFCNSAVCEHCDPCTCKKHGIEECTLTSTNPKCKEEDSRSLPLWCL 179
QY 175 ILVLLIPLVFIYRKRYKRCWKRRQDDPSRTSSRETIPMNASLSKYIPRIADMTI 234
DB 180 LLLLPVIVVWIKKCKRKRKENGPHSTYLNPT-AINLSDVLSKYITTIAGMTL 238
QY 235 QEAKKFARENKIEGKIDIMHSDIQTAEQVOLLWCYQSHGKSDAYQDLIKGLKAE 294
DB 239 SQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQVOLLRNWYQLHGKDKACDTLIKGLTAD 298
QY 295 CRTLDKFDQVQKLGKSTPDGTGNEG 323
DB 299 LCTLAEKIHAVILKDI---TSDTENSNGF 324

RESULT 5
Q9BDP2 Q9BDP2 PRELIMINARY; PRT; 333 AA.
AC Q9BDP2
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE FAS antigen CD95.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -.
DR HSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 45.8%; Score 825.5; DB 6; Length 331;
Best Local Similarity 49.8%; Pred. No. 2.7e-65;
Matches 164; Conservative 46; Mismatches 108; Indels 11; Gaps 5;

QY 1 MLWTWAVPLVLAGSQLR-----VHTQGTNSISLSKLRRVHETDKNCSGLYOGGPGFC 55
DB 1 MLGIWTLPLVLT-YVRLLSKCVNAQVTDISSKGFELRKIVTTIETQNLGLHHEGQFC 59
QY 56 CQCPQCKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRTCLDDEHGLEVEYTC 115
DB 60 RNPCCPGERKARDCTVNEDEPDCVPCQEGEYTDKGHFSKRCRLCDEGHGLEVEINC 119
QY 116 TLQNTCKCKPDYCDSPGCEHCVCASCHEGTLEPCTATSNTRKQSPRNL-WLLT 174
DB 120 TRQNTCKCRKPNFCNSAVCEHCDPCTCKKHGIEECTLTSTNPKCKEEDSRSLPLWCL 179
QY 175 ILVLLIPLVFIYRKRYKRCWKRRQDDPSRTSSRETIPMNASLSKYIPRIADMTI 234
DB 180 LLLLPVIVVWIKKCKRKRKENGPHSTYLNPT-AINLSDVLSKYITTIAGMTL 238
QY 235 QEAKKFARENKIEGKIDIMHSDIQTAEQVOLLWCYQSHGKSDAYQDLIKGLKAE 294
DB 239 SQVKDFVRKNGVSEAKIDEIKNDNVQDTAEQVOLLRNWYQLHGKDKACDTLIKGLTAD 298
QY 295 CRTLDKFDQVQKLGKSTPDGTGNEG 323
DB 299 LCTLAEKIHAVILKDI---TSDTENSNGF 324

RESULT 6
Q9TV79 Q9TV79 PRELIMINARY; PRT; 319 AA.
AC Q9TV79
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE B-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX Isono T., Tanbe Y., Nagano Y., Seto A.;
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Db 1 MLGIWTLTLVLKFLGLSTSVNAQVTDINPKGLELRKVTJAJETONLEDOYYVGFCHK 60
QY 58 PCOPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYNCTL 117
Db 61 PCSPGKKKARDCTVDDDEPCVQCGEYTDKSHSPKRCRCRLCDEHGLEVEINCTR 120
QY 118 TQNTKCKCKPDDFYCDSPGCEHCVRASCCEHGTLEPCTATSNTRCKQSPR-NRLWLLTL 176
Db 121 TQNTKCRCPNFCNSAVCEHCDPCTCEHGIKECSLTSNAKCKEEGFRANLLWLLCL- 179
QY 177 VLIP-LVFIYKRYKRRKCKRRQDDPESRTSSRETIPMNASNLSKYIPRIAEADMTIQ 235
Db 180 -LLVPILLIIVWVIRCKRHRRENGHRETTINSETVPMNLSDVLSKYITVIAEHMTIS 238
QY 236 EAKKFARENNIEGKIDEIMHDSIODTAEQVOLLCLWYQSHGSDAYQDLIKGLKAKC 295
Db 239 QVRDFVRKNGVNEAKIDEIKNDNIQDTAEQVOLLRNWYQLHGKDAYDTLLNGLKANKL 298
QY 296 RRTLDKFDQVMDKLGKSTPDGTGNE 322
Db 299 TALVEKIQNIKDSSENSNRQNEQ 325

RESULT 2
Q9TSN4 PRELIMINARY; PRT; 331 AA.
AC Q9TSN4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Death receptor Fas (APO-1/CD95).
GN FAS.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20237686; PubMed=10773350;
RA Murayama Y., Terao K., Inoue-Murayama M.;
RT "Molecular cloning and characterization of cynomolgus monkey Fas.";
RL Hum. Immunol. 61:474-485(2000).
DR EMBL; AB031420; BAA83551.1;
DR HSSP; P25445; IDDF
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR SMART; SM00208; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 331 AA; 37265 MW; 0C617508081B05DF CRC64;

Query Match 46.3%; Score 835; DB 6; Length 331;
Best Local Similarity 49.7%; Pred. No. 3.8e-66;
Matches 165; Conservative 47; Mismatches 112; Indels 8; Gaps 4;

QY 1 MLMIWAVLPLVLAGSOLR-----VHTQGTNSISSESLKLRVHETDKNCSGLYQGGPPC 55
Db 1 MLGIWTLPLVT-SVRLSLKCNVAQVTDISSKGFELRKIVTTIETQNLGLHHEGQFC 59
QY 56 COPCPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYNCT 115
Db 60 RNPCCPGERKARDCTVNEDEPCVQCGEYTDKSHSPKRCRCRLCDEHGLEVEINCTR 119
QY 116 TLTQNTKCKCKPDDFYCDSPGCEHCVRASCCEHGTLEPCTATSNTRCKQSPR-NRLW 174
Db 120 TRTQNTKCRCKPDDFYCDSPGCEHCVRASCCEHGTLEPCTATSNTRCKQSPR-NRLW 174

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QY 175 ILVLLIPLVFIYKRYKRRKCKRRQDDPESRTSSRETIPMNASNLSKYIPRIAEADMTI 234
Db 180 LLLIIPPIVVIWIKKACRKHRENGHRETTINPET-AINLSDVLSKYITTIAGAWTL 238
QY 235 QEAKFARENNIEGKIDEIMHDSIODTAEQVOLLCLWYQSHGSDAYQDLIKGLKAE 294
Db 239 SQVKDFVRKNGVNEAKIDEIKNDNIQDTAEQVOLLRNWYQLHGKDAYDTLLNGLKAD 298
QY 295 CRTLDKFDQVMDKLGKSTPDGTGNEQQL 326
Db 299 LCTLAEKIHAVILKIDTSDTENSFRNEIOSL 330

RESULT 3
Q9XS29 PRELIMINARY; PRT; 320 AA.
AC Q9XS29;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE C-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=5986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021299; BAA78431.1;
DR EMBL; AB021296; BAA78428.1;
DR HSSP; P25445; IDDF
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;

Query Match 46.0%; Score 829.5; DB 6; Length 320;
Best Local Similarity 50.3%; Pred. No. 1.1e-65;
Matches 169; Conservative 43; Mismatches 97; Indels 27; Gaps 7;

QY 1 MLMIWAVLPLVLAGSOLRVTHTQGTNSISSESLKLRVHETDKNCSGLYQGGPPCQPCQ 60
Db 1 MTGIWVLLPLIL-----TCIAGSLSTINDCKIKNETQYSTG---YLSGNFCCQLCP 49
QY 61 PGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEYNCTLTQ 120
Db 50 PGTKKADCTSNEGKPDCEPCQEGEYTDKSHSPKRCRCRLCDEHGLEVEYDCTTIQ 109
QY 121 TKCKCPDDFYCDSPGCEHCVRASCCEHGTLEPCTATSNTRCKQ-----SPRNLWLLTI 175
Db 110 TKCRCSNFFCNALCKEHCPCCTMCEHGIIECTQTSNTKCKEKGSTGSKHFLWLLCI 169
QY 176 LVLLIPLVFIYKRYKRRKCKRRQDDPESRTSSRETIPMNASNLSKYIPRIAEADMTIQ 235
Db 170 L-LLIPIVIGLRKRYKRRKCKRRQDDPESRTSSRETIPMNASNLSKYIPTIAEEMKIN 236
QY 236 EAKKFARENNIEGKIDEIMHDSIODTAEQVOLLCLWYQSHGSDAYQDLIKGLKAE 295
Db 227 EVKEFVRKNGVNEAKIDEIKNDNIQDTAEQVOLLRNWYQLHGKDAYDTLLNGLKANKL 286
QY 296 RRTLDKFDQVMDKLGKSTPDGTGNE-----ENEGQCL 326
Db 287 CALAEKIQDIQVOKDI---TSDHNDLDIRDEKERQSL 319

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:00:40 ; Search time 28.6495 Seconds
(without alignments)
2351.779 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804

Sequence: 1 MLWIWAVLPLVLAGSQLRVH.....KDLGKSTPTDGNENEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTEMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	839.5	46.5	328	6 Q9BDP0	Q9bdp0 aotus trivi
2	835	46.3	331	6 Q9TSN4	Q9tsn4 macaca fasc
3	829.5	46.0	320	6 Q9XS29	Q9xs29 oryctolagus
4	825.5	45.8	331	6 Q9BDN0	Q9bdn0 macaca neme
5	822.5	45.6	333	6 Q9BDP2	Q9bdp2 macaca mula
6	820	45.5	319	6 Q9TV79	Q9tv79 oryctolagus
7	816.5	45.3	331	6 Q9BDN4	Q9bdn4 cercocobus
8	815	45.2	334	6 Q9GL40	Q9gl40 macaca mula
9	802.5	44.5	331	6 Q9GK36	Q9gk36 macaca assa
10	802	44.5	327	6 Q97491	Q97491 ovis aries
11	768	42.6	310	6 Q9GK28	Q9gk28 macaca arct
12	609.5	33.8	150	11 Q9R230	Q9r230 rattus norv
13	520.5	28.9	263	6 Q9XS60	Q9xs60 oryctolagus
14	438	24.3	312	13 Q9DGH8	Q9dgh8 gallus gall
15	428.5	23.8	285	13 Q9DGH7	Q9dgh7 gallus gall
16	416	23.1	147	6 Q8SQ52	Q8sq52 felis silve

17	380.5	21.1	124	6	Q8SQ51	Q8sq51 felis silve
18	242.5	13.4	357	13	Q9DF34	Q9df34 brachydanio
19	240	13.3	65	6	Q8SQ49	Q8sq49 felis silve
20	228.5	12.7	438	13	Q9DFV0	Q9dfv0 brachydanio
21	205.5	11.4	283	6	Q9XS28	Q9xs28 cercopithec
22	202.5	11.2	276	13	Q9DD2	Q9ddd2 gallus gall
23	198.5	11.0	267	6	O02764	O02764 oryctolagus
24	197	10.9	387	13	Q9PVD4	Q9pvd4 xenopus lae
25	179.5	10.0	368	13	Q9IAR7	Q9iar7 gallus gall
26	179.5	10.0	401	13	Q9PRG7	Q9prg7 xenopus lae
27	178.5	9.9	387	11	Q8VD70	Q8vd70 mus musculu
28	177.5	9.8	368	13	Q9FW79	Q9fw79 gallus gall
29	174	9.6	326	12	O57122	O57122 cowpox viru
30	172	9.5	351	12	O73559	O73559 cowpox viru
31	170	9.4	169	11	O9JKE0	O9jke0 rattus norv
32	170	9.4	413	11	Q99MM1	Q99mm1 mus musculu
33	168.5	9.3	347	12	O57119	O57119 cowpox viru
34	168.5	9.3	349	12	O57305	O57305 cowpox viru
35	168.5	9.3	351	12	O57121	O57121 cowpox viru
36	168.5	9.3	360	12	O57118	O57118 cowpox viru
37	168	9.3	349	12	O57098	O57098 camelopox vi
38	168	9.3	349	12	O8UYA7	O8uya7 camelopox vi
39	168	9.3	349	12	O57284	O57284 camelopox vi
40	168	9.3	351	12	O57117	O57117 cowpox viru
41	167.5	9.3	347	12	O57115	O57115 cowpox viru
42	167.5	9.3	355	12	O85308	O85308 cowpox viru
43	165.5	9.2	350	12	O57123	O57123 cowpox viru
44	165	9.1	326	12	O57120	O57120 cowpox viru
45	165	9.1	349	12	O57111	O57111 variola vir

ALIGNMENTS

RESULT 1

Q9BDP0 ID Q9BDP0 PRELIMINARY; PRT; 328 AA.

AC Q9BDP0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE FAS antigen CD95.

OS Aotus trivirgatus (Night monkey) (Douroucoul).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=9505;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21383618; PubMed=11491535;

RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,

RA Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing, and homology analysis of nonhuman primate

RT Fas/Fas-ligand and co-stimulatory molecules."

RL Immunogenetics 53:315-328(2001).

DR EMBL; AF344835; AAK37531.1; -;

DR HSPB; P25445; IDDF.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR_c6; 2.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00017; DEATH DOMAIN; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00050; TNFR_NGFR_2; 2.

DR VARIANT 157

FT SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match 46.5%; Score 839.5; DB 6; Length 328;

Best Local Similarity 50.2%; Pred. No. 1.5e-66;

Matches 164; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

QY 1 MLWIWAVLPLVL---AGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGPFCCQ 57

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:58:17 ; Search time 15.3127 seconds
(without alignments)
885.720 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804
Sequence: 1 MLWIAVPLVLVAGSQLRVH.....KDLGKSTPDGTGNEGQCLE 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	327	1	TNR6_MOUSE
2	1058.5	58.7	324	1	TNR6_RAT
3	856	47.5	335	1	TNR6_HUMAN
4	841.5	46.6	332	1	TNR6_PIG
5	814	45.1	323	1	TNR6_BOVIN
6	272	15.1	381	1	T10B_MOUSE
7	215	11.9	468	1	T10A_HUMAN
8	205	11.4	176	1	TR23_MOUSE
9	203.5	11.3	283	1	TR14_HUMAN
10	202	11.2	272	1	TNR4_MOUSE
11	196	10.9	417	1	TR12_HUMAN
12	194.5	10.8	277	1	TNR5_HUMAN
13	189.5	10.5	455	1	TR1A_HUMAN
14	185	10.3	454	1	TR1A_MOUSE
15	183	10.1	180	1	TR22_MOUSE
16	179.5	10.0	435	1	TNR3_HUMAN
17	179.5	10.0	440	1	T10B_HUMAN
18	179.5	10.0	435	1	T10B_MOUSE
19	179	9.9	461	1	TR1A_RAT
20	178	9.9	260	1	TNR7_HUMAN
21	172	9.5	351	1	CRMB_COMPX
22	171	9.5	277	1	TNR4_HUMAN
23	169	9.4	461	1	TR1A_PIG
24	168	9.3	349	1	CRMB_CAMPS
25	167	9.3	250	1	TNR7_MOUSE
26	166.5	9.2	386	1	T10D_HUMAN
27	165.5	9.2	416	1	TR16_CHICK
28	165	9.1	289	1	TNR5_MOUSE
29	163	9.0	259	1	T10C_HUMAN
30	163	9.0	349	1	CRMB_VARV
31	161	8.9	471	1	TR1A_BOVIN
32	155.5	8.6	269	1	TNR5_BOVIN
33	155.5	8.6	300	1	TR6B_HUMAN

34	154.5	8.6	425	1	TR16_RAT
35	154.5	8.6	595	1	TNR8_HUMAN
36	154	8.5	415	1	TNR3_MOUSE
37	148	8.2	461	1	TR1B_HUMAN
38	144	8.0	401	1	T11B_HUMAN
39	144	8.0	401	1	T11B_RAT
40	143	7.9	401	1	T11B_MOUSE
41	143	7.9	417	1	TR16_MOUSE
42	141	7.8	427	1	TR16_HUMAN
43	139	7.7	297	1	XEDA_HUMAN
44	128.5	7.1	616	1	TR11_HUMAN
45	127.5	7.1	687	1	VS41_GIALA

ALIGNMENTS

RESULT 1
TNR6_MOUSE
ID TNR6_MOUSE STANDARD; PRT; 327 AA.
AC P25446; O9DC01;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
(CD95).
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92148151; PubMed-1371136;
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
mouse Fas antigen".
J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-129/SV;
RA Koczan D., Ibrahim S.M., Thiesen H.J.;
RT "Role of a mutant fas receptor in a transgenic mouse".
Submitted (JUL-2000) to the EMBL/GenBank/DBAJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6J; TISSUE-Kidney;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection".
Nature 405:685-690(2001).
RN [4]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE-93189576; PubMed-7680478;

RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
 RT "Aberrant transcription caused by the insertion of an early
 RT transposable element in an intron of the Fas antigen gene of lpr
 RL mice.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
 RN [5]
 RP VARIANT LPR
 RX MEDLINE-92195401; PubMed-1372394;
 RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
 RA Nagata S.;
 RT "Lymphoproliferation disorder in mice explained by defects in Fas
 RT antigen that mediates apoptosis.";
 RL Nature 356:314-317(1992).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
 CC LIVER, LUNG, HEART, AND ADULT OVARY.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- DISEASE: DEFECS IN TNFSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
 CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
 CC PRODUCTION.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL; M83649; AAA37593.1; -;
 DR EMBL; AK002590; BAB22211.1; -;
 DR EMBL; AJ295702; CAC00638.1; -;
 DR EMBL; AJ295703; CAC00638.1; JOINED.
 DR EMBL; AJ295704; CAC00638.1; JOINED.
 DR EMBL; S56490; AAB25700.1; -;
 DR EMBL; S56485; AAB25700.1; JOINED.
 DR EMBL; S56486; AAB25700.1; JOINED.
 DR PIR; A46484; A46484.
 DR HSP; P25445; 1DDF.
 DR MGD; MG1:95484; Tnfrsf6.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001388; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR Pfam; PF00531; death; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Disease mutation.
 FT SIGNAL 1 21
 FT CHAIN 22 327
 FT DOMAIN 22 169
 FT TRANSMEM 170 186
 FT DOMAIN 187 327
 FT REPEAT 43 79
 FT REPEAT 80 123
 FT REPEAT 124 162
 FT DOMAIN 222 306
 FT DISULFID 44 55
 FT BY SIMILARITY.

FT DISULFID 56 69 BY SIMILARITY.
 FT DISULFID 59 78 BY SIMILARITY.
 FT DISULFID 81 97 BY SIMILARITY.
 FT DISULFID 100 115 BY SIMILARITY.
 FT DISULFID 103 123 BY SIMILARITY.
 FT DISULFID 125 139 BY SIMILARITY.
 FT DISULFID 142 153 BY SIMILARITY.
 FT DISULFID 145 161 BY SIMILARITY.
 FT CARBOHYD 43 43
 FT CARBOHYD 114 114
 FT VARIANT 246 246
 FT CONFLICT 38 38 H -> R (IN LPR).
 SQ SEQUENCE 327 AA; 37418 MW; F6BFEC5ACE356EEE CRC64;
 Query Match 100.0%; Score 1804; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1e-133;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPCCPCQ 60
 Db 1 MLWTWAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSEGLYQGGPCCPCQ 60
 QY 61 PGKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
 Db 61 PGKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVEINCTLTQN 120
 QY 121 TKCKCKPDFCDSPGCEHCYRCASCEHGTLEPCTATNTNCRKQSPNRNLWLLTILVLI 180
 Db 121 TKCKCKPDFCDSPGCEHCYRCASCEHGTLEPCTATNTNCRKQSPNRNLWLLTILVLI 180
 QY 181 PLVFIYKRYKRWKRRQDDPSRSTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
 Db 181 PLVFIYKRYKRWKRRQDDPSRSTSSRETIPMNASNLSLSKYIPRIADMTIOEAKKF 240
 QY 241 ARENNKEGIDEIMHDSIQDTAEQVQLLLCWYQSHGSKSDAYQDILKGLKAECRRTLD 300
 Db 241 ARENNKEGIDEIMHDSIQDTAEQVQLLLCWYQSHGSKSDAYQDILKGLKAECRRTLD 300
 QY 301 KFDQVMQKDLGKSTPDPTGNEGQCLE 327
 Db 301 KFDQVMQKDLGKSTPDPTGNEGQCLE 327
 RESULT 2
 TNFR6_RAT
 ID TNFR6_RAT STANDARD; PRT; 324 AA.
 AC Q63199;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
 DE (CD95).
 GN TNFRSF6 OR PT1 OR FAS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE-94128114; PubMed-7507668;
 RA Kimura K., Yamamoto M., Wakatsuki T.;
 RT "A variant mRNA species encoding a truncated form of Fas antigen in
 RT the rat liver.";
 RL Biochem. Biophys. Res. Commun. 198:666-674(1994).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or

[illegible]

Db	115	NCTRTRNTKCRCKSNFFCNSSPCEHCNCPCTTCEHGIEIKCTPTSNTKCGKSRSHANSLWA	174
QY	173	LTLVLVLLPIVFYRYRKRCWKRRDDPESTTSRETIPMNASNLUSKYIPRIADQM	232
Db	175	L--LILLIPLVIIYYKWSRERNKKNDYCNSAASNDGRLNLTDVLGKYIPTSAEQM	232
QY	233	TIOEAKKFARENNIKGGKTDEIMHDSIQDTAEQKVOLLICWTQSHGKSDAYODLTGLKK	292
Db	233	RITEVKFEVRKNGMEEAKTDDIMHDNVHETAEOKVOLLRNWYQSHGKNKNACTLTLSLPK	292
QY	293	AECRRITLDKQDMVQDLGKSTPDGTGNNEGQCL	326
Db	293	A-----LAECTCDIVMKDITNERENANQLONENL	322

RESULT 6	
110B_MOUSE	
ID	T10B_MOUSE
TT	STANDARD;
AC	Q9QZM4; Q9JIL5; Q9JIL6;
DC	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (MK).
DE	
GN	TNFRSF10B OR DR5 OR KILLER.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
	[1]
RP	SEQUENCE FROM N.A.
RP	

receptor 5) (WK).
TNFRSF10B OR DR5 OR KILLER.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99310501; PubMed=10383128;
RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of
the (TRAIL)/DR5 tumor necrosis factor-related apoptosis-inducing ligand
(TRAIL) death receptor.";
RT Cancer Res. 59:2770-2775(1999).
RL [2]
SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nakamura Y., Tamari M., Watanabe O.;
RT "Mouse TRAIL receptor.";
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
adaptor molecule FADD recruits caspase-8 to the activated
receptor. The resulting death-inducing signaling complex (DISC)
performs caspase-8 proteolytic activation which initiates the
subsequent cascade of caspases (aspartate-specific cysteine
proteases) mediating apoptosis. Promotes the activation of NF-
kappaB.
CC
-!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By
similarity).
CC
-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
-!- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC
-!- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC
-!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN
CC

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 CC CC -----
 DR DR EMBL; AF176833; RAD52656.1; - -
 DR DR EMBL; AB031081; BAA96462.1; - -
 DR DR EMBL; AB031082; BAA96463.1; - -
 DR DR HSSP; O14763; 1D0G.
 DR DR MGD; MGI:1341090; Tnf1rs10b.


```

FT REPEAT 147 188
FT REPEAT 189 229
FT DOMAIN 365 448
FT REPEAT 29 32
FT POLY-ALA
FT DISULFID 132 145
FT BY SIMILARITY
FT DISULFID 148 164
FT BY SIMILARITY
FT DISULFID 167 180
FT BY SIMILARITY
FT DISULFID 170 188
FT BY SIMILARITY
FT DISULFID 207 221
FT BY SIMILARITY
FT DISULFID 211 229
FT BY SIMILARITY
FT CARBOHYD 156 156
FT N-LINKED (GLCNAC...) (POTENTIAL)
FT CONFLICT 141 141
FT H -> R (IN REF. 1)
FT CONFLICT 209 209
FT R -> T (IN REF. 1)
SQ SEQUENCE 468 AA; 50061 MW; 7E9661859A550CD4 CRC64;

Query Match 11.9%; Score 215; DB 1; Length 468;
Best Local Similarity 21.1%; Pred. No. 1.3e-09;
Matches 82; Conservative 64; Mismatches 137; Indels 106; Gaps 16;

QY 13 AGSQLRVH-----TQGTNISESLKLRVRVHETDKNCKSEGLYQGGFFCCQPCQP 61
DB 82 ASPLRVHKTFFVGVVGLQVVPSSAATIKLH-----DQSIGTQQWEHSP-L-GEICPP 134
QY 62 GKKKVEDCKMNGGTPCAPCTEGKEYMDKNHYADKRCRTLCDEHGLEVETNCTLTQNT 121
DB 135 GSHRSEH-----PGACNRCCTEGVYTNASNNLFACLPCTACKSDS--EERSPCCTTTRNT 186
QY 122 KCKKPDFYCDSPGCEHVCRA--SCEHG--TLEPCTATSTNCC--RKQSPNRLWLTLTIL 176
DB 187 ACQCKPGFTFRNDNAEMCRKSCRGWVKVDCCTPWSIDIECVKHSNGHNTWILVV 246
QY 177 VLLPLVFIY-----RKYRKCKWKR--RQDDPESRTSSRTTIPMNASNL 219
DB 247 TLVPLLVAVLVVCCIGSGCGDPRKMDRVCFWRLGLLPGGAEDNAHNEILLSNADSL 306
QY 220 S-----LSKYIPRIADMTIQ-----EAK----- 238
DB 307 STFFSEQMESQEPADLTGVTVSPGEAQLLGPAEAGSQRRLVLPANGADPTETLML 366
QY 239 ---KFA-----RNNIKEGKIDEIMHDSIODTAEQKVLQLLCWYQSHGSKDAY 283
DB 367 FFDKFNATVPDSDWQMLRQLDLTKNEID--VVRAGTAGPDGALYAMLKMKVNTGRNASI 425
QY 284 QDLKGLKKAECRTLDKFDQVQKDLGK 312
DB 426 HTLLDALERMEERHAKEIKQDLL--VDSGK 453

RESULT 8
TR23_MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHC0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN TNFRSF23 OR TNFRSF11 OR TNFRH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN-129/Sv; TISSUE-Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region: Implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]

RP SEQUENCE FROM N.A.
RA Pan G., Mao W., Rissler P.;
RT "Characterization of SOB, a member of the TNFR family.";
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -|- TISSUE SPECIFICITY: Ubiquitous
CC -|- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; AJ278264; CAC16405.1; -
CC EMBL; AJ276505; CAC27352.1; -
CC EMBL; AY046550; AAL05072.1; -
CC HSSP; P19438; 1EXT.
CC MGSD; MGI:1930269; Tnfrsf23.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 3.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00050; TNFR_NGFR_2; 2.
CC RECEPTOR; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 9
FT TRANSMEM 10 30
FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT REPEAT 31 176
FT REPEAT 37 72
FT TNFR-CYS 1.
FT REPEAT 74 114
FT TNFR-CYS 2.
FT REPEAT 115 155
FT TNFR-CYS 3.
FT DISULFID 38 49
FT BY SIMILARITY.
FT DISULFID 50 63
FT BY SIMILARITY.
FT DISULFID 53 72
FT BY SIMILARITY.
FT DISULFID 75 90
FT BY SIMILARITY.
FT DISULFID 93 106
FT BY SIMILARITY.
FT DISULFID 96 114
FT BY SIMILARITY.
FT DISULFID 116 131
FT BY SIMILARITY.
FT DISULFID 134 147
FT BY SIMILARITY.
FT DISULFID 137 155
FT BY SIMILARITY.
FT CARBOHYD 148 148
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DB7D CRC64;

Query Match 11.4%; Score 205; DB 1; Length 176;
Best Local Similarity 31.5%; Pred. No. 2.6e-09;
Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

QY 43 NCSEGLYQGGPCCQPCQPKKKKVEDCKKNGGTPCAPCTEGKEYMDKNHYADKRCRCTL 102
DB 37 NCPDGEYQSDVCCCKTSPSGTFVKAPCKIPHTQGCCKHPG-TFTGKDNGLHDLCLST 95
QY 103 CDEEHGLEVETNCTLTQNTKCKKPD-FYCDSPGCEHVCRCASCEHG--TLEPCTATSN 159
DB 96 CKDKQNWAD--CSATSDRCKCQGLYYDPKFPESCRCPTCKCPGIPVLQECNSTANT 153
QY 160 NCRK--QSPNRLWLTLTILVLLI 180
DB 154 VCSSSVSNPRNLLMLLVFCI 176

RESULT 9
TR14_HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q96J31; Q8WXR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2) (TR2).
DE
GN TNFRSF14 OR HVEM OR HVEA.
```


FT DISULFID 63 77 BY SIMILARITY.
FT DISULFID 80 95 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 123 BY SIMILARITY.
FT DISULFID 126 139 BY SIMILARITY.
FT DISULFID 145 164 BY SIMILARITY.
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 11.28; Score 202; DB 1; Length 272;
Best Local Similarity 26.38; Pred. No. 7.3e-09;
Matches 69; Conservative 22; Mismatches 85; Indels 84; Gaps 12;

QY 2 LNIWAVLPLVLAGSQLRVHTQGTNSISLKLRRRVHETDKNCSGLYQGGPFCCQPCQP 61
DB 1 MYWVQOPTALL---LLALTLGVTA-----RRL-----NCVKHTYPSGHKCCRECQP 44

QY 62 GKKVDECKNGGPTCAPCTEGKEYMDKNHYADKRCRTCLDDEHGLEVTNCTLTQNT 121
DB 45 GHGMVSRCDHTRDT-LCHPCETG-FYNEAVNY-DTCRQCTQCNHRSGSELKQNCPTQDT 101

QY 122 KCKKPDFY-----CD---SPG---CEHCVRG----- 142
DB 102 VCRPCGTQPRDSGYKLGVDVCPGPHSPGNACKPWTNCTLSGKQTRHPASDGLD 161

QY 143 ASCE-----HGTLEPCATSNCRKQS-----PRNLWLTLIL 176
DB 162 AVCEDRSLLATLWETQRTFRPTTVQSTTWPRTELSPPTLTPGPAFVLLGLGL 221

QY 177 VLLIPLVFIYKRYKRCWK 196
DB 222 GLLAPLTVLLALYLLKAWR 241

RESULT 12

TR12_HUMAN
ID TR12_HUMAN STANDARD; PRT; 417 AA.
AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;
AC Q99830; Q9BY86; Q14865; Q14866; Q00275; Q00276; Q00277; Q00278;
AC Q00279; Q00280; Q9UME0; Q9UME1; Q9UME5;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 12 precursor
DE (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-
DE mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)
DE (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated
DE receptor of death) (LARD).
GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
RX TISSUE=Lymphoid;
RC MEDLINE=97088617; PubMed=8934525;
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA Grinham C.J., Brown R., Farrow S.N.;
RA "A death-domain-containing receptor that mediates apoptosis.";
RL Nature 384:372-375(1996).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=97081063; PubMed=8875942;
RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
RT "Signal transduction by DR3, a death domain-containing receptor
RL related to TNFR-1 and CD95.";
RL Science 274:990-992(1996).
[3]
RN SEQUENCE FROM N.A.
CC

RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=97148200; PubMed=8994832;
RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA Goddard A.D., Bauer K.D., Ashkenazi A.;
RT "Apo-3, a new member of the tumor necrosis factor receptor family,
RT contains a death domain and activates apoptosis and NF-kappa-B.";
RL Curr. Biol. 6:1669-1676(1996).
[5]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
RX MEDLINE=9727273; PubMed=9114039;
RA Sreaton G.F., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
[6]
RN SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
RX MEDLINE=98113360; PubMed=9446802;
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and a non-Hodgkin's lymphomas.";
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
[7]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[8]
RN SEQUENCE OF 4-417 FROM N.A.
RC TISSUE=Brain, and Retal lung;
RX MEDLINE=97205335; PubMed=9052839;
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA Browning J.L., Macdonald H.R., Tschopp J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL Immunity 6:79-88(1997).
[9]
RN SEQUENCE OF 7-417 FROM N.A.
RC TISSUE=Brain;
RA Chaudhary P.M., Hood L.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly
CC with the adaptor TRADD. Mediates activation of NF-kappaB and
CC induces apoptosis. May play a role in regulating lymphocyte
CC homeostasis.
CC -1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
CC (Potential).
CC -1- ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE),
CC 2/LARD-1B, 3/WSL-S1/LARD-3, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11,
CC 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND
CC 12/BETA SOLUBLE; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -1- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
CC residue instead of arginine.

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Db 196 VVIPILFILLVLVFIKKVAKK 221

RESULT 14

TRIA_HUMAN STANDARD: PRT: 455 AA.

AC P19438;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1A precursor (p50)

DE (TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor

DE binding protein 1 (TNFRI)]

GN TNFRSF1A OR TNFRI OR TNFAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=90235284; PubMed=2158863;

RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,

RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;

RT "Molecular cloning and expression of a receptor for human tumor

RT necrosis factor.";

RT Cell 61:361-370(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=90235284; PubMed=2158862;

RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,

RA Tabuchi H., Lesslauer W.;

RT "Molecular cloning and expression of the human 55 kd tumor necrosis

RT factor receptor.";

RT Cell 61:351-359(1990).

RN [3]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.

RX MEDLINE=91006021; PubMed=1698610;

RA Nohar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,

RA Aderka D., Holtmann H., Wallach D.;

RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA

RT for the type I TNF-R, cloned using amino acid sequence data of its

RT soluble form, encodes both the cell surface and a soluble form of the

RT receptor.";

RL EMBL J. 9:3269-3278(1990).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=9100841; PubMed=1702293;

RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,

RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;

RT "Molecular cloning and expression of human and rat tumor necrosis

RT factor receptor chain (p60) and its soluble derivative, tumor

RT necrosis factor-binding protein.";

RL DNA Cell Biol. 9:705-715(1990).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=91017509; PubMed=2170974;

RA Gray P.W., Barrett K., Chantray D., Turner M., Feldman M.;

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and

RT expression of recombinant soluble TNF-binding protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=92250049; PubMed=1315717;

RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;

RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and

RT localization to chromosome 12p13.";

RL Genomics 13:219-224(1992).

RN [7]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RA Strausberg R.;

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[8]

RL SEQUENCE OF 41-45.

RP MEDLINE=90110215; PubMed=2153136;

RA Engelmann H., Novick D., Wallach D.;

RT "Two tumor necrosis factor-binding proteins purified from human

RT urine. Evidence for immunological cross-reactivity with cell surface

RT tumor necrosis factor receptors.";

RL J. Biol. Chem. 265:1531-1536(1990).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.

RX MEDLINE=93258809; PubMed=8387891;

RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,

RA Broger C., Loetscher H., Lesslauer W.;

RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF

RT beta complex: Implications for TNF receptor activation.";

RL Cell 73:431-445(1993).

RN [10]

RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.

RX MEDLINE=97094982; PubMed=8939750;

RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;

RT "Structures of the extracellular domain of the type I tumor necrosis

RT factor receptor.";

RL Structure 4:1251-1262(1996).

RN [11]

RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.

RX MEDLINE=99213501; PubMed=10199409;

RA McDermott M.F., Aksentjevich I., Galon J., McDermott E.M.,

RA Ogunkolade B.W., Centola M., Mansfield E., Gadin M., Karenko L.,

RA Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,

RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,

RA Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,

RA Mulvey J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,

RA Hitman G.A., O'Shea J., Kastner D.L.;

RT "Germline mutations in the extracellular domains of the 55 kDa TNF

RT receptor, TNFR1, define a family of dominantly inherited

RT autoinflammatory syndromes.";

RL Cell 97:133-144(1999).

RN [12]

RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric

RP TNFSF1/lymphotxin-alpha. The adaptor molecule FADD recruits

RP caspase-8 to the activated receptor. The resulting death-inducing

RP signaling complex (DISC) performs caspase-8 proteolytic activation

RP which initiates the subsequent cascade of caspases (aspartate-

RP specific cysteine proteases) mediating apoptosis. Contributes to

RP the induction of noncytotoxic TNF effects including anti-viral

RP state and activation of the acid sphingomyelinase.

RP SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

RP HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

RP PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

RP WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

RP PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

RP TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

RP ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

RP NF-KAPPA B SIGNALING.

RP SUBCELLULAR LOCATION: Type I membrane protein and secreted.

RP DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO

RP THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH

RP NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

RP PTM: The soluble form is produced from the membrane form by

RP proteolytic processing.

RP DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant

RP familial hibernian fever (FHF), a disease characterized by

RP recurrent fever, abdominal pain, localized tender skin lesions and

RP myalgia.

RP SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

RP SIMILARITY: CONTAINS 1 DEATH DOMAIN.

RP DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".

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SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60468; AAA39751.1; -;
DR EMBL; M59377; AAA40464.1; -;
DR EMBL; X59238; CAA41922.1; -;
DR EMBL; X57796; CAA40936.1; -;
DR EMBL; L26349; AAA59361.1; -;
DR EMBL; M76656; AAA40465.1; -;
DR EMBL; M88067; AAA40465.1; JOINED.
DR EMBL; M76655; AAA40465.1; JOINED.
DR PIR; A38634; GQMST1.
DR PIR; S16677; S16677.
DR PIR; S19021; S19021.
DR HSP; P19438; 1EXT.
DR MGD; MGI:131484; Tnftrsf1a.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR Pfam; PF00531; death; 1.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 1A.
FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 235 POTENTIAL.
FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 441 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.

FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 394 394 R -> G (IN REF. 6).
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;
Query Match 10.3%; Score 185; DB 1; Length 454;
Best Local Similarity 29.2%; Pred. No. 2.7e-07;
Matches 47; Conservative 20; Mismatches 84; Indels 10; Gaps 5;
QY 7 VLPVLVLAGSQLRVHTQGTNISESLKLRVRRVHETDKNCSEGLY---OGGPFCCQCPQPGK 63
Db 10 LLSLVLLALLMGIIHPSGVTLGLVPSLGDREK---RDSLCPQGVVHSHKNNISCTCKCHKGT 66
QY 64 KVEDCKMNGTPTCAPCTEGKEYMDKNHYADKRCRRCTLCDEEHGLEVETNCTLTQNTKC 123
Db 67 YLVSDCPSGRDVTVCRECEKG-TFTASQNYLRQCLSCCTCKKEMSQVEISPCQADKDTVC 125
QY 124 KCKPDFYCDSPGCEH--CVRCASCEHGTLE-PCITATNTNC 161
Db 126 GCENQFQRYLSETHFQVDCSPCFNGTVPCKEITQNTVC 166

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Job time : 17.3127 secs

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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:57:39 ; Search time 55.6647 Seconds
(without alignments)
801.926 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MLGIWTLPLVLTSLSS.....KDTSDSENFRNEIQSLV 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_101002.*
- 1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
 - 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
 - 6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
 - 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
 - 8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
 - 9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
 - 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
 - 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
 - 16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
 - 17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
 - 18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
 - 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	335	13 AAR28084	Human cell surface
2	1804	100.0	335	16 AAR78606	Human Fas protein.
3	1804	100.0	335	17 AAR9681	Human Fas antigen.
4	1804	100.0	335	17 AAR92528	hFas from plasmid
5	1804	100.0	335	18 AAW50289	Human Fas antigen.
6	1804	100.0	335	19 AAW49104	Fas protein. Mamm
7	1804	100.0	335	21 AAB19341	Amino acid encodin
8	1804	100.0	335	21 AAB01335	CD-95 (FAS/APO-1)
9	1804	100.0	335	22 AAB50517	Human tumour necro
10	1804	100.0	669	19 AAW64484	Human TNFR1 protei

11	1792	99.3	335	21	AAB36267	Human Fas receptor
12	1743	96.6	331	22	AAR50893	Human Fas receptor
13	1667.5	92.4	314	16	AAR76238	Fas-delta-TM. Hom
14	1667.5	92.4	314	17	AAR9682	Human Fas soluble
15	1655.5	91.8	314	20	AAW98070	Soluble Fas recept
16	1484	82.3	281	21	AAB26982	Human Fas. Homo s
17	1225	67.9	219	22	AAB66978	Fas protein. Unid
18	997	55.3	237	21	AAB53420	Human colon cancer
19	972	53.9	173	21	AAB36229	Human Fas receptor
20	966	53.5	600	16	AAR78610	Expression vector
21	956	53.0	600	17	AAR92526	Fas antigen #1. S
22	870.5	48.3	927	22	AAV97653	Flk-1extrafasTm/cy
23	857.5	47.5	436	21	AAV91026	Apoptobody3sc fusi
24	856	47.5	327	14	AAR41688	Murine Fas. Mus m
25	856	47.5	327	16	AAR78611	Murine Fas antigen
26	856	47.5	327	17	AAR92530	mFas sequence. Sy
27	856	47.5	327	21	AAB19344	Amino acid sequenc
28	852	47.2	327	20	AAW86241	Flt-1extrafasTm/cy
29	852	47.2	920	22	AAV97652	Human Fas antigen
30	811.5	45.0	144	18	AAW50286	Human Fas antigen
31	811.5	45.0	159	18	AAW50288	Human Fas antigen
32	811.5	45.0	376	18	AAW50287	Antigenic peptide
33	811.5	45.0	376	19	AAW60037	CD44hextrafasTm/cy
34	806.5	44.7	431	22	AAV97650	CD44hextra/tmFasCy
35	751	41.6	436	22	AAV97651	Human Fas soluble
36	621.5	34.5	149	17	AAR9683	Human Fas soluble
37	599	32.6	121	23	ABR81752	Tumour necrosis fa
38	557	30.9	111	23	ABR81750	Tumour necrosis fa
39	535.5	29.7	170	21	AAB36228	Rat Fas receptor.
40	534.5	29.6	576	16	AAR78613	Expression vector
41	530	29.4	169	16	AAR78612	Plasmid fragment p
42	526.5	29.2	592	17	AAR92527	Fas antigen #2. S
43	427	23.7	84	22	AAV97654	Fas/Apo-1/CD95 Dea
44	425	23.6	84	19	AAW62178	Fas-R protein frag
45	352	19.5	68	20	AAW93611	Human Fas/apoi pro

ALIGNMENTS

RESULT 1
AAR28084
ID AAR28084 standard; Protein; 335 AA.
AC AC
AAR28084;
DT 12-MAR-1993 (first entry)
XX Human cell surface antigen.
DE Fas antigen; apoptosis; pF58; NGFR/TNFR family.
KW Homo sapiens.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT Protein /label= signal
FT Protein 17..335
FT Modified-site /label= Fas_antigen
FT Modified-site 118..120
FT Modified-site /label= N-glycosylation_site
FT Modified-site /note= "putative"
FT Modified-site 136..138
FT Modified-site /label= N-glycosylation_site
FT Modified-site /note= "putative"
FT Domain 174..190
FT Domain /label= transmembrane
FT Domain 17..173
FT Domain /label= extracellular
FT Domain /note= "cysteine-rich"
FT Domain 191..335
FT Domain /label= cytoplasmic
XX

PN EP510691-A.
 XX 28-OCT-1992.
 XX 24-APR-1992; 92EP-0107060.
 XX 26-APR-1991; 91JP-0125234.
 XX (OSAB-) OSAKA BIOSCIENCE INST.
 PA Itoh N, Nagata S, Yonehara S;
 PI WPI; 1992-358914/44.
 DR N-PSDB; AAQ29959.
 XX
 XX DNA encoding human cell surface antigen - used to clarify
 PT apoptosis mechanism of various types of cell, and to prepare
 PT monoclonal antibodies that react with tumour cells expressing Fas
 XX
 XX Claim 3; Fig 1 and 2; 27pp; English.
 XX The Fas antigen is implicated in apoptosis. A cDNA clone encoding
 CC the antigen was isolated (pf58) and the amino acid sequence of Fas
 CC was deduced from it. The mature protein has a calculated mol.wt. of
 CC 36,000 and is a member of the NGFR/TNFR family of cell-surface
 CC membrane proteins. The inventors claim a protein comprising at
 CC least the extracellular domain of Fas antigen.
 XX
 SQ Sequence 335 AA;
 Query Match 100.0%; Score 1804; DB 13; Length 335;
 Best Local Similarity 100.0%; Pred. No. 2.4e-151;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 DB 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 QY 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDEGHGVEINCT 120
 DB 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDEGHGVEINCT 120
 QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 DB 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 QY 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAINLSVDLSKYITTTIAGVM 240
 DB 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAINLSVDLSKYITTTIAGVM 240
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTLIKDLKK 300
 DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTLIKDLKK 300
 QY 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 DB 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 RESULT 2
 ID AAR78606
 XX AAR78606 standard; Protein; 335 AA.
 AC AAR78606;
 XX
 DT 19-FEB-1996 (first entry)
 XX
 DE Human Fas protein.
 XX
 XX Plasmid pf58; human Fas cDNA; soluble membrane protein;
 KW antibody production; diseases; treatment; prevention.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..16
 FT /label= sig_peptide
 FT Peptide 17..335
 FT /label= mat_peptide
 XX JP07115988-A.
 XX 09-MAY-1995.
 XX 26-OCT-1993; 93JP-0267644.
 XX 26-OCT-1993; 93JP-0267644.
 XX (NISR) JAPAN TOBACCO INC.
 XX WPI; 1995-202847/27.
 XX N-PSDB; AAQ95297.
 XX Preparation of soluble membrane proteins - for their use in antibody
 PT production for the treatment and prevention of related diseases
 XX
 XX Example 1; Pages 15-17; 51pp; Japanese.
 XX AAR78606 (human Fas protein) is encoded by the plasmid pf58 which
 CC contains hfas cDNA. The plasmid was used in the construction of an
 CC expression vector for the prodn. of recombinant soluble membrane
 CC proteins. The proteins can be used in antibody prodn. for the
 CC treatment and prevention of related diseases.
 XX
 SQ Sequence 335 AA;
 Query Match 100.0%; Score 1804; DB 16; Length 335;
 Best Local Similarity 100.0%; Pred. No. 2.4e-151;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 DB 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 QY 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDEGHGVEINCT 120
 DB 61 KPCCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDEGHGVEINCT 120
 QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 DB 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCEGSRSLNLGLCLL 180
 QY 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAINLSVDLSKYITTTIAGVM 240
 DB 181 LLPPLIVVVKRKEVQKTCRKHKKENQSGHESPTLNPETVAINLSVDLSKYITTTIAGVM 240
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTLIKDLKK 300
 DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNWHQHGKKEAYDTLIKDLKK 300
 QY 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 DB 301 ANLCTLAEKIQTILKIDTSDSENSFRNEIOSLV 335
 RESULT 3
 ID AAR99681
 XX AAR99681 standard; Protein; 335 AA.
 AC AAR99681;
 XX
 DT 10-OCT-1996 (first entry)
 XX Human Fas antigen.
 DE
 XX Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
 KW

KW angioimmunoblastic lymphadenopathy; AILD.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..16
FT /label= sig_peptide
FT Protein 17..335
FT /label= Mat_protein
FT Domain 17..173
FT /label= Extracellular_domain
FT Domain 174..190
FT /label= Transmembrane_domain
FT Domain 191..335
FT /label= Cytoplasmic_tail
XX
PN WO9620206-A1.
XX
XX 04-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17083.
XX
XX 23-DEC-1994; 94US-0371263.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Cheng J, Liu C, Mountz JD, Zhou T;
XX
XX WPI; 1996-321796/32.
XX N-PSDB; AAT34526.
XX
XX Natural, soluble form of Fas antigen secreted by human cells is
PT result of alternative mRNA processing - used to diagnose
PT Fas-associated disease, e.g. systemic lupus erythematosus
XX
PS Disclosure; Page 109-111; 152pp; English.
XX
XX A cDNA clone (AAT34526) codes for a membrane receptor-like protein,
CC Fas antigen (AAR99681). It was isolated from cDNA derived from the
CC peripheral blood mononuclear cells of systemic lupus erythematosus
CC (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients. 4
CC Soluble variants (AAR99682-85) were identified of the Fas antigen.
CC These arose by alternative splicing of Fas gene transcripts. The
CC Fas variants were present at higher levels in SLE and AILD patients
CC than the non-soluble Fas antigen.
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDGHGVEINCT 120
QY 121 RPTQNTKCRCKPNFFCNSTVCEHCDPTCKCEHGIIEKCTILTSNTKCEGSRNLGWLCLL 180
DB 121 RPTQNTKCRCKPNFFCNSTVCEHCDPTCKCEHGIIEKCTILTSNTKCEGSRNLGWLCLL 180
QY 181 LLPILPIVWKKKEVQKTCRKHKENQGSHPPTLNPTVAINLSDVLSKYITTIAGVM 240
DB 181 LLPILPIVWKKKEVQKTCRKHKENQGSHPPTLNPTVAINLSDVLSKYITTIAGVM 240
QY 241 TISQVKGFFVRKGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQHGKKEAYDTLLKDKK 300
DB 241 TISQVKGFFVRKGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQHGKKEAYDTLLKDKK 300
QY 301 ANLCTLAERKIQTIIILKDTSDSENSFRNEIQSLV 335

DB 301 ANLCTLAERKIQTIIILKDTSDSENSFRNEIQSLV 335
RESULT 4
AAR92528
ID AAR92528 standard; Protein; 335 AA.
XX
XX AAR92528;
XX
XX 06-SEP-1996 (first entry)
XX hFas from plasmid pCEV4/hFas.
XX
XX Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT 1..16
FT /note= "hFas signal peptide"
FT Protein 17..335
FT /note= "mature hFas"
XX
XX WO9601277-A1.
XX
XX 18-JAN-1996.
XX
XX 03-MAR-1995; 95WO-JP00349.
XX
XX 14-FEB-1995; 95JP-0025637.
XX 06-JUL-1994; 94JP-0154706.
XX
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX (NISB) JAPAN TOBACCO INC.
XX
XX Hachiya T, Noguchi J, Yonehara S;
XX WPI; 1996-087635/09.
XX N-PSDB; AAT16303.
XX
XX Immunoassay method for soluble Fas antigen in body fluids - for
PT diagnosis of auto-immune diseases such as rheumatoid arthritis and
PT systemic lupus erythematosus
XX
XX Example 8; Page 49-52; 124pp; Japanese.
XX
XX This sequence represents the sequence for the human Fas antigen contained
CC within the Plasmid pCEV4/hFas. The soluble Fas antigen is included in
CC the immunoassay kit of the invention. The kit is for the assay of
CC soluble Fas antigen and contains an immobilised anti-soluble Fas
CC monoclonal antibody, as well as the standard soluble Fas antigen
CC represented by this sequence. The assay is simple and has high accuracy,
CC high sensitivity, and is capable of assaying a number of different
CC specimens at the same time. The immunoassay is used on biological
CC samples (such as serum) and is useful for diagnosis of autoimmune
CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
CC (SLE).
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDGHGVEINCT 120

QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSVDVLSKYITTIAGVM 240
DB 181 LLPIPLIYVWKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSVDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHLGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHLGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335

RESULT 5
AAW50289
ID AAW50289 standard; Protein; 335 AA.
XX
AC AAW50289;
XX
DT 16-JUL-1998 (first entry)
XX
DE Human Fas antigen.
XX
KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
KW apoptosis modulation.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..16
FT Peptide /label= sig_peptide
FT Peptide 17..335
FT Peptide /label= mat_peptide
FT Region 17..173
FT /note= "claimed fragment"
XX
PN WO9742319-A1.
XX
PD 13-NOV-1997.
XX
PF 01-MAY-1997; 97WO-JP01502.
XX
PR 02-MAY-1996; 96JP-0135760.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (OSAB) OSAKA BIOSCIENCE INST.
XX
PI Nagata S, Nakamura N;
XX
XX WPI; 1997-558981/51.
DR N-PSDB; AAV07002.
XX
XX
PT Fas antigen derivative containing modified extracellular region -
PT has low antigenicity, promotes apoptosis and is useful in treatment
PT of viral and other diseases
XX
PS Claim 2; Fig 1-2; 102pp; Japanese.
XX
XX
CC The present sequence was used in the development of novel Fas
CC antigen derivatives, which contain a Fas antigen extracellular
CC region lacking one or more amino acid residues in the region from
CC the amino-terminal to (but excluding) the 1st cysteine residue
CC (preferably at least 29 residues are deleted).
CC The derivatives are effective regulators of apoptosis and can be
CC used (either by administration of the polypeptide, or by the use
CC of the coding DNA in gene therapy) to treat a range of diseases,
CC e.g. diabetes, arthritis, lupus and in particular viral diseases
CC

CC such as hepatitis, influenza and HIV, by modulating apoptosis of
CC virus-infected cells.
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 18; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLWTLLPLVLTAVRLSSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGOFCH 60
DB 1 MGLWTLLPLVLTAVRLSSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGOFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCEGHLEVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSVDVLSKYITTIAGVM 240
DB 181 LLPIPLIYVWKRKEVQKTCRKRKENGSHESPTLNPTETVAINLSVDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHLGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHHQHLGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETKIQTIIILKDTSDSENSNFRNEIQSLV 335

RESULT 6
AAW49104
ID AAW49104 standard; Protein; 335 AA.
XX
AC AAW49104;
XX
DT 18-NOV-1998 (first entry)
XX
DE Fas protein.
XX
KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
KW prophylactic; AIDS.
XX
OS Mammalia sp.
XX

FH Key Location/Qualifiers
FT Peptide 1..16
FT Peptide /note= "Signal peptide"
FT Protein 17..335
FT Protein /note= "Fas protein"
FT Region 17..172
FT /note= "The portion of a Fas protein which can be
FT fused to a Fc polypeptide to form a Fas-Fc
FT fusion protein"
XX
PN WO9835692-A1.
XX
PD 20-AUG-1998.
XX
PF 17-FEB-1998; 98WO-GB00485.
XX
PR 17-FEB-1997; 97GB-0003276.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Screamon GR, Xu X;
XX

DR WPI; 1998-456867/39.
XX N-PSDB; AAV32993.
PT Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
PT diseases - by interfering with interaction of Fas with Fas-ligand
PT expressed on activated CD4+ cells, e.g. cells infected with HIV
XX
XX Disclosure; Fig 7; 71pp; English.
XX
XX The present sequence represents a Fas protein sequence used in the
CC method of the invention. The method is concerned with reducing
CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
CC cells in an immune cell population which also comprises of Fas-ligand
CC (FasL)-expressing activated CD4+ cells. It involves contacting this
CC immune cell population with an effective amount of an agent (e.g. a
CC soluble Fas-FC fusion protein) which would interfere with the
CC interaction between Fas and FasL. Therefore, the method is useful for
CC identifying suitable agents which can reduce depletion of activated
CC Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
CC is the use of the agent in the manufacture of therapeutic compositions.
CC Apoptosis of lymphocytes can be triggered by the interaction of the
CC cell surface receptor Fas and its ligand FasL. By interfering with
CC this interaction, the method described and its preparations can prevent
CC apoptosis of CD8+ TK lymphocytes caused by expression of FasL on
CC activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
CC especially the result of CD4+ cell infection with an immunodeficiency
CC virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
CC virus (SIV). The claimed prevention of apoptosis may then allow
CC maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
CC towards the CD4+ cells infected with the infectious agent, enabling
CC treatment (prophylactic and/or therapeutic) of immunodeficiency
CC diseases e.g. AIDS.
XX
XX Sequence 335 AA;

Query Match 100.0%; Score 1804; DB 19; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Qy 181 LLPIPLIVVVRKKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIVVVRKKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQTIILKDTSDSENSNFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIILKDTSDSENSNFRNEIQSLV 335

RESULT 7
AAB19341
ID AAB19341 standard; Protein; 335 AA.
XX
XX AAB19341;
XX
XX 06-MAR-2001 (first entry)
XX
XX Amino acid encoding a human Fas (Apo-1) protein.

XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;
KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
KW autoimmune disease; inflammatory disease; lymphoma.
XX
XX Homo sapiens.
XX
XX WO200061150-A1.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US09540.
XX
XX 12-APR-1999; 99US-0290640.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean NM, Marcusson EG;
XX
XX WPI; 2000-628395/60.
XX
XX N-PSDB; AAC61798.
XX
XX Antisense oligonucleotides for treating hepatitis and colon, liver or
PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT 1 (Fap-1) expression
XX
XX Example 2; Page 73-74; 116pp; English.
XX
XX The present sequence represents human Fas (Apo-1). The specification
CC describes antisense compounds which are targeted to the 5'-untranslated
CC region, translational start site, translational termination region
CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
CC phosphatase). The antisense compounds are used to inhibit the
CC expression of Fas, FasL or Fap-1 in cells or tissues. They are used
CC to treat autoimmune or inflammatory diseases such as hepatitis. They
CC can also be used to treat cancer, especially colon, liver or lung
CC cancer or lymphoma.
XX
XX Sequence 335 AA;

Query Match 100.0%; Score 1804; DB 21; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Qy 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGSRNLGWLCLL 180
Qy 181 LLPIPLIVVVRKKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIVVVRKKEVQKTCRKHRENQSGHESPTLNPTETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNHLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQTIILKDTSDSENSNFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIILKDTSDSENSNFRNEIQSLV 335

RESULT 8
AAB01335
ID AAB01335 standard; Protein; 335 AA.

XX AAB01335;
XX 25-SEP-2000 (first entry).
DT CD-95 (FAS/APO-1) death receptor.
XX
DE
XX UL144; death receptor; apoptosis; programmed cell death; FAS;
KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW human.
XX
XX Homo sapiens.
OS
XX WO200034335-A2.
PN
XX 15-JUN-2000.
XX
XX 03-DEC-1999; 99WO-US26035.
PF
XX 04-DEC-1998; 98US-0205018.
PR
XX (SCHE) SCHERING CORP.
PA
XX Leong C, Phillips JH;
PI
XX WPI; 2000-423383/36.
DR
XX
XX Purified or recombinant polypeptide for modulating apoptosis comprises
PT a sequence which binds to an antibody specific for UL144 or its
PT fragments
XX
XX Disclosure; Page 64-65; 76pp; English.
PS
XX
XX A pure or recombinant polypeptide which binds to a polyclonal antibody
CC specific for the mature UL144 is useful for screening molecules which
CC block induction of apoptosis or interfere with antiapoptotic activity.
CC The polypeptide is also useful for modulating apoptosis and useful in
CC treatment of conditions associated with abnormal physiology or
CC development, such as cancer or degenerative conditions and for
CC regulation of viral infection and replication. At least five
CC different death receptors are known, which include the CD95
CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX
XX Sequence 335 AA;
SQ
Query Match 100.0%; Score 1804; DB 21; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 M LGIWTLLPLVLTSVARLSKSNVAQVTDINSGLELRKVTVTQNLGLHHDGQFCH 60
DB 1 M LGIWTLLPLVLTSVARLSKSNVAQVTDINSGLELRKVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRLCDEGHLEVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHSSKRCRLCDEGHLEVEINCT 120
QY 121 RTQNTKCRCKPNFCNTVCEHDCPCKCEHGIKECTLFSNTKCKEGRSRLGLCLL 180
DB 121 RTQNTKCRCKPNFCNTVCEHDCPCKCEHGIKECTLFSNTKCKEGRSRLGLCLL 180
QY 181 LLPLPLVWKRKEVQTKRHKRKNQSGHESPTLPETVAINLSVDLSKYTTTAGVM 240
DB 181 LLPLPLVWKRKEVQTKRHKRKNQSGHESPTLPETVAINLSVDLSKYTTTAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEINDNVQDTAEQKVOLLRNHQLHGKKEAYDTLLKDLKK 300
DB 241 TLSQVGFVRKNGVNEAKIDEINDNVQDTAEQKVOLLRNHQLHGKKEAYDTLLKDLKK 300
QY 301 ANCLTAEKIQTILKIDITSSENSNFRNEIOSLV 335
|||||

DB 301 ANCLTAEKIQTILKIDITSSENSNFRNEIOSLV 335
RESULT 9
ID AAB50517 standard; Protein; 335 AA.
XX
XX AAB50517;
XX AC
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor FAS protein SEQ ID NO:7.
XX
KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
XX Homo sapiens.
OS
XX WO2000071150-A1.
PN
XX 30-NOV-2000.
PD
XX 18-MAY-2000; 2000WO-US13515.
PF
XX 20-MAY-1999; 99US-0135164.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Wei Y, Ruben SM, Gentz RL, Ni J;
XX WPI; 2001-041051/05.
DR
XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
XX Disclosure; Fig 2; 285pp; English.
PS
XX
CC The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities and can be used in gene therapy. The TRID polynucleotides
CC are useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TRID in the exemplification of the present invention.
XX
SQ Sequence 335 AA;
Query Match 100.0%; Score 1804; DB 22; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.4e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTETQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDGEGHGLEVEINCT 120
Qy 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWLCCL 180
Db 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWLCCL 180
Qy 181 LLPIPLIIVWKRKEVQKTCRKRKRNQSGHSPETNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIIVWKRKEVQKTCRKRKRNQSGHSPETNPETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQTIIKIDITSSENSFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIIKIDITSSENSFRNEIQSLV 335
RESULT 10
AAW64484
ID AAW64484 standard; Protein; 669 AA.
AC AAW64484;
XX XX
DT 20-OCT-1998 (first entry)
DE Human TNFR1 protein.
KW Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;
KW agonist; tumour necrosis factor; TNF; ligand; autoimmune disease;
KW infection; graft rejection; antagonist; inhibitor; diagnostic.
XX XX
OS Homo sapiens.
XX XX
PN WO982856-A1.
XX XX
PD 30-JUL-1998.
XX XX
PF 27-JAN-1998; 98WO-US01464.
XX XX
PR 05-FEB-1997; 97US-0037829.
PR 28-JAN-1997; 97US-0035722.
XX XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX XX
PI Dixit VM, Gentz RL, Ni J, Pan JG, Rosen CA;
XX XX
DR WPI; 1998-427952/36.
XX XX
PT Nucleic acid encoding human death domain-containing receptor 4 -
PT useful for therapeutic modulation of apoptosis, in e.g. cancer and
PT autoimmune diseases
XX XX
PS Disclosure; Fig 2; 92pp; English.
XX XX
CC This sequence represents a human tumour necrosis factor receptor-1 which
CC is used in a method resulting in the isolation of a human death domain
CC containing receptor 4, DR4. DR4 agonists are used to increase apoptosis
CC induced by tumour necrosis factor (TNF)-family ligands, e.g. in cases of
CC cancer, autoimmune disease, viral or other infections, inflammation,
CC graft vs. host disease, acute or chronic graft rejection. Antagonists of
CC DR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune
CC deficiency syndrome, neurodegenerative disease, myelodysplastic syndrome,
CC ischaemic injury, toxin-induced liver damage, septic shock, cachexia and
CC anorexia, also a wide range of inflammatory conditions. DR4 of fragments

CC of the protein are used diagnostically, e.g. to detect mutant forms of
CC DR4 (possibly associated with disease), for isolating the DR4 gene or
CC related sequences and for chromosomal mapping.
XX XX
SQ Sequence 669 AA;
Query Match 100.0%; Score 1804; DB 19; Length 669;
Best Local Similarity 100.0%; Pred. No. 6.1e-151;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKKTVTVTETQNLGLHHDGQFCH 60
Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRRLCDGEGHGLEVEINCT 120
Qy 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWLCCL 180
Db 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWLCCL 180
Qy 181 LLPIPLIIVWKRKEVQKTCRKRKRNQSGHSPETNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIIVWKRKEVQKTCRKRKRNQSGHSPETNPETVAINLSDVLSKYITTIAGVM 240
Qy 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFEVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQHLGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIQTIIKIDITSSENSFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIIKIDITSSENSFRNEIQSLV 335
RESULT 11
AAB36267
ID AAB36267 standard; Protein; 335 AA.
XX XX
AC AAB36267;
XX XX
DT 20-FEB-2001 (first entry)
DE Human Fas receptor.
XX XX
KW Human; death domain containing receptor; DR3-VL; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.
XX XX
OS Homo sapiens.
XX XX
PN WO200064465-A1.
XX XX
PD 02-NOV-2000.
XX XX
PF 21-APR-2000; 2000WO-US10741.
XX XX
PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENTZ) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX XX
DR WPI; 2000-687263/67.
XX XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an

PT autoimmune disease comprising administering an antibody to Death Domain
 PT Containing Receptor proteins and a second therapeutic agent -
 PS Disclosure; Fig 3; 273pp; English.

XX The present invention provides the protein and coding sequences for two
 CC death domain containing receptors, designated DR3 and DR3-VI. These
 CC receptors are involved in apoptosis, and the sequences given can be used
 CC in the treatment of cancers, infections, cardiovascular disorders such as
 CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
 CC and congenital heart defects, neurodegenerative diseases including
 CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
 CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
 CC and to promote angiogenesis and wound healing.

SQ Sequence 335 AA;

Query Match 99.3%; Score 1792; DB 21; Length 335;
 Best Local Similarity 99.7%; Pred. No. 2.8e-150;
 Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 DB 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 120
 DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 120
 QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWCLL 180
 DB 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWCLL 180
 QY 181 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 240
 DB 181 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 240
 QY 241 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 300
 DB 241 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 300
 QY 301 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 335
 DB 301 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 335

RESULT 12

ID AAB50893
 XX AAB50893 standard; Protein; 331 AA.

AC AAB50893;

DT 19-MAR-2001 (first entry)

DE Human Fas receptor.

XX Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective;
 KW antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant;
 KW vasotrophic; antiallergic; antidiabetic; vulnerary; ophthalmological;
 KW antiviral; antibacterial; antifungal; antiparasitic; gene therapy;
 KW tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder;
 KW apoptosis; cardiovascular disorder; inflammatory disease; wound;
 KW infection; neurological disease; Fas receptor; protein coordinate data.

OS Homo sapiens.

XX WO200073321-A1.

PN 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14554.

XX 28-MAY-1999; 99US-0136786.

PR

PR 07-JUL-1999; 99US-0142563.
 PR 15-JUL-1999; 99US-0144023.
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ni J;

XX WPI; 2001-025250/03.

XX Nucleic acid encoding a tumor necrosis factor receptor 10, useful in
 PT the diagnosis, treatment or prevention of cancer, autoimmune disorders,
 PT and diseases and disorders associated with apoptosis -
 XX Disclosure; Fig 2; 212pp; English.

XX The present sequence is given in a specification relating to an isolated
 CC nucleic acid encoding a human tumour necrosis factor receptor TR10.
 CC The TR10 polynucleotide, polypeptide, antibodies, agonists and
 CC antagonists are useful in the diagnosis, treatment or prevention of
 CC cancer, such as breast and ovarian cancer and leukaemia; autoimmune
 CC disorders such as multiple sclerosis, Crohn's disease and graft versus
 CC host disease; diseases associated with increased apoptosis such as AIDS,
 CC Alzheimer's disease and Parkinson's disease; cardiovascular disorders
 CC such as limb ischaemia and congenital heart defects; inflammatory
 CC diseases e.g. allergy; wound healing; disorders associated with
 CC neovascularisation, e.g. diabetic retinopathy; infectious diseases such
 CC as viral, bacterial, fungal and parasitic infections; and neurological
 CC diseases such as amyotrophic lateral sclerosis.

SQ Sequence 331 AA;

Query Match 96.6%; Score 1743; DB 22; Length 331;
 Best Local Similarity 98.8%; Pred. No. 6e-146;
 Matches 331; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
 QY 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 60
 DB 1 MGIWTLPLVLTSSVARLSKSVNAQVTDINSKGLRLKTVTTVETQNLGLHHDGQFCH 59
 QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 120
 DB 60 -PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRLCDEGHGVEINCT 118
 QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWCLL 180
 DB 119 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTCKEGRSRLGLWCLL 177
 QY 181 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 240
 DB 178 LLPIPLIVWVKRKEVQKTCRKHKRKNQSGSHESPTLNPEVAINLSDVLSKYITTTAGVM 237
 QY 241 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 300
 DB 238 TISQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHGKKEAYDTLIKDLKK 297
 QY 301 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 335
 DB 298 ANLCTLAETIQLTKDITSDSENSFRNEIOSLV 331

RESULT 13

AAR76238

ID AAR76238 standard; Protein; 314 AA.

XX AAR76238;

DT 06-NOV-1995 (first entry)

DE Fas-delta-TM.

XX Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
 KW adoptive immunotherapy; transgenic animal.

```
OS XX Homo sapiens.
FH XX Key Location/Qualifiers
FT XX Peptide 1..16
FT XX /label= Sig_peptide
PN XX WO9513701-A.
XX XX
XX XX 26-MAY-1995.
XX XX
XX XX 15-NOV-1994; 94WO-US13173.
XX XX
XX XX 15-NOV-1993; 93US-0152443.
XX XX
XX XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX XX
XX XX Barr PJ, Kiefer MC, Shapiro JP;
XX XX
XX XX WPI; 1995-200120/26.
XX XX N-PSDB; AAQ93879.
XX XX
XX XX New nucleic acid encoding Fas protein without its trans-membrane region
XX XX - and related vectors, transformed cells, transgenic animals, protein and
XX XX antibodies, useful for control of Fas mediated apoptosis
XX XX
XX XX Claim 9; Fig.3-1 to 3-4; 38pp; English.
XX XX
XX XX mRNA was obtd. from human lymphocytes and PCR was used to make
XX XX cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
XX XX region) mRNA. The PCR product was ligated into phuescript and the
XX XX recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
XX XX insert sequence of pBluescript-Fas-delta-TM encoded the protein
XX XX given in AAR76238.
XX XX
XX XX Sequence 314 AA;

Query Match 92.4%; Score 1667.5; DB 16; Length 314;
Best Local Similarity 93.7%; Pred. No. 2.7e-139;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60

Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120

Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLGLCLL 180
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKCKE----- 168

Qy 181 LLPTPLIIVVRKEVQKTCRKHRENQSHESPTLNPTETVAINLSVDLSKYITTIAGVM 240
Db 169 -----VRRKEVQKTCRKHRENQSHESPTLNPTETVAINLSVDLSKYITTIAGVM 219

Qy 241 TLSQVKGVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNHQLHGKKEAYDTLLKDLKK 300
Db 220 TLSQVKGVRKNGVNEAKIDEIKNDNVODTAQKQVOLLRNHQLHGKKEAYDTLLKDLKK 279

Qy 301 ANLCTLAEKIQTIIILKIDITSSENSFRNEIQSLV 335
Db 280 ANLCTLAEKIQTIIILKIDITSSENSFRNEIQSLV 314

RESULT 14
AAR99682
ID AAR99682 standard; Protein; 314 AA.
XX AAR99682;
XX
XX 10-OCT-1996 (first entry)
XX
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```
DE XX Human Fas soluble antigen Fas dell.
XX XX
KW XX Fas antigen: autoimmune disease; systemic lupus erythematosus; SLE;
XX XX angioimmunoblastic lymphadenopathy; AILD.
XX XX
OS XX Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX XX Peptide 1..16
XX XX /label= Sig_peptide
XX XX Protein 17..314
XX XX /label= Mat_protein
XX XX /note= "soluble Fas dell antigen"
XX XX Domain 17..168
XX XX /label= Extracellular_domain
XX XX /note= "the 5 C-terminal residues of the
XX XX Fas antigen extracellular domain are
XX XX deleted in Fas dell"
XX XX Domain 169..314
XX XX /label= Cytoplasmic_domain
XX XX Peptide 164..173
XX XX /note= "preferred peptide from breakpoint region
XX XX (claim 4, page 132)"
XX XX Peptide 164..174
XX XX /note= "preferred peptide from breakpoint region"
XX XX Peptide 161..171
XX XX /note= "preferred peptide from breakpoint region"
XX XX WO9620206-A1.
XX XX 04-JUL-1996.
XX XX 22-DEC-1995; 95WO-US17083.
XX XX 23-DEC-1994; 94US-0371263.
XX XX (UABR-) UAB RES FOUND.
XX XX Cheng J, Liu C, Mountz JD, Zhou T;
XX XX WPI; 1996-321796/32.
XX XX N-PSDB; AAT34527.
XX XX
XX XX Natural, soluble form of Fas antigen secreted by human cells is
XX XX result of alternative mRNA processing - used to diagnose
XX XX Fas-associated disease, e.g. systemic lupus erythematosus
XX XX
XX XX Claim 4; Page 114-16; 152pp; English.
XX XX
XX XX A natural, soluble Fas antigen variant (AAR99682), designated Fas
XX XX dell, and other Fas variants (AAR99683-85) are derived by alternative
XX XX splicing of Fas gene transcripts. A cDNA clone (AAT34527) coding for
XX XX the variant was obtd. from human peripheral blood mononuclear cells.
XX XX The Fas dell variant lacks the transmembrane domain of insoluble
XX XX Fas antigen (AAR99681). Recombinant dell variant, or fragments of
XX XX it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.
XX XX Detection of increased levels of soluble forms of Fas antigen can
XX XX be used to diagnose autoimmune diseases, esp. systemic lupus
XX XX erythematosus and angioimmunoblastic lymphadenopathy.
XX XX
XX XX Sequence 314 AA;

Query Match 92.4%; Score 1667.5; DB 17; Length 314;
Best Local Similarity 93.7%; Pred. No. 2.7e-139;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60

Qy 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDCDGHGVEINCT 120
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QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKEGRSNLWGLCLL 180
 Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKE----- 168
 QY 181 LLPIPLIIVWKRKEVQKTCRKHKENQSGHESPTLNPEVAINLSDVDLSKIYITTIAGVM 240
 Db 169 -----VKRKEVQKTCRKHKENQSGHESPTLNPEVAINLSDVDLSKIYITTIAGVM 219
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
 Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 279
 QY 301 ANLCTLAEKIQTILKDTSDSENSNFRNEIOSLV 335
 Db 280 ANLCTLAEKIQTILKDTSDSENSNFRNEIOSLV 314

RESULT 15
 AAW98070
 ID AAW98070 standard; Protein; 314 AA.
 AC AAW98070;
 DT 21-JUN-1999 (first entry)
 DE Soluble Fas receptor.
 KW Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;
 KW graft versus host disease; autoimmune disease; psoriasis;
 KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy.
 OS Mammalia.

Key Location/Qualifiers
 Peptide 1..16
 Protein /note= "signal peptide" 17..314
 /note= "mature protein" 109
 Misc-difference /note= "encoded by GAA" 118
 Modified-site /note= "N-glycosylated"
 W09903999-A1.
 28-JAN-1999.
 16-JUL-1998; 98WO-US14771.
 17-JUL-1997; 97US-0052829.
 (UNMI) UNIV MICHIGAN.
 Chen J, Nabel GJ;
 WPI; 1999-132243/11.
 N-PSDB; AAX24878.
 Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host disease or autoimmune disease
 Disclosure; Fig 4B; 7lpp; English.

This present sequence is a soluble Fas receptor. The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (FasL). In some embodiments, an FasL is coadministered with the immunosuppressive agent, and the cell mixture comprises neutrophil cells. The method can be practised in vitro, ex vivo or in vivo. Suitable immunosuppressive agents include antisense molecules that inhibit

CC endogenous FasL expression, soluble Fas receptors or variants, ribozymes that inhibit the endogenous expression of FasL, drugs that inhibit FasL signalling, agents that induce the endogenous expression of transforming growth factor (TGF)-beta, and polynucleotides coding for an immunosuppressive agent such as TGF-beta. The method can be used for treating diseases associated with an undesired FasL-mediated proinflammatory response, e.g. graft versus host disease, or an autoimmune disease such as systemic lupus erythematosus, rheumatoid arthritis and psoriasis. The invention also provides a method for identifying agents which modulate FasL stimulation of a proinflammatory response.

XX Sequence 314 AA;

Query Match 91.8%; Score 1655.5; DB 20; Length 314;
 Best Local Similarity 93.1%; Pred. No. 3.le-138;
 Matches 312; Conservative 0; Mismatches 2; Indels 21; Gaps 1;

QY 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKKTVTVTETQNLGLHHDGQFCH 60
 Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLERKKTVTVTETQNLGLHHDGQFCH 60
 QY 61 KCPGPKERKARDCTVNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDCDEGHLEVEINCT 120
 Db 61 KCPGPKERKARDCTCNGDEPCVPCQEGKEYTDKAHFSSKRCRCLDCDEGHLEVEINCT 120
 QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKEGRSNLWGLCLL 180
 Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKTLTSTNTKCKE----- 168
 QY 181 LLPIPLIIVWKRKEVQKTCRKHKENQSGHESPTLNPEVAINLSDVDLSKIYITTIAGVM 240
 Db 169 -----VKRKEVQKTCRKHKENQSGHESPTLNPEVAINLSDVDLSKIYITTIAGVM 219
 QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
 Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 279
 QY 301 ANLCTLAEKIQTILKDTSDSENSNFRNEIOSLV 335
 Db 280 ANLCTLAEKIQTILKDTSDSENSNFRNEIOSLV 314

Search completed: May 9, 2003, 17:05:04
 Job time : 57.6647 secs

QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHIKECTLTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVWVRKEVQKTCRKRKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIVWVRKEVQKTCRKRKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIQTIIILKDIITSDSENFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIIILKDIITSDSENFRNEIQSLV 335

RESULT 2

US-08-409-338-1
; Sequence 1, Application US/08409338
; Patent No. 5891434

GENERAL INFORMATION:

; APPLICANT: Kramer, Peter H.
; APPLICANT: Debatin, Klaus-Michael
; APPLICANT: Trauth, Bernhard C.
; APPLICANT: Behrmann, Iris
; APPLICANT: Dhein, Jens
; APPLICANT: Klas, Christiane
; APPLICANT: M ller, Peter
; APPLICANT: Falk, Werner
; APPLICANT: Oehm Alexander
; APPLICANT: Daniel, Peter T.
; TITLE OF INVENTION: Monoclonal Antibodies to the Apo-1 Antigen
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington, MA 02173
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/409,338
; FILING DATE:

CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,644
; FILING DATE: 16-JUN-1994
; APPLICATION NUMBER: US 07/691,016
; FILING DATE: 17-JUN-1991
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CTR89-35A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-409-338-1

Query Match 100.0%; Score 1804; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGFCH 60
Db 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHIKECTLTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVWVRKEVQKTCRKRKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIVWVRKEVQKTCRKRKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIQTIIILKDIITSDSENFRNEIQSLV 335
Db 301 ANLCTLAEKIQTIIILKDIITSDSENFRNEIQSLV 335

RESULT 3

US-09-290-640-2
; Sequence 2, Application US/09290640
; Patent No. 6204055

GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussan, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-290-640-2

Query Match 100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGFCH 60
Db 1 MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHIKECTLTNTKCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTCKEHIKECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVWVRKEVQKTCRKRKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIVWVRKEVQKTCRKRKENOGSHESPTLNPEVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300

Qy 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335
|||||
Db 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335

RESULT 4
US-09-006-353A-7
: Sequence 7, Application US/09006353A
: Patent No. 6261801
: GENERAL INFORMATION:
: APPLICANT: WEI, YING-FEI
: APPLICANT: YU, GUO-LIANG
: APPLICANT: GENTZ, REINER
: APPLICANT: RUBEN, STEVEN
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: US
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/006,353A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOKES, ANDERS A
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PF341
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 335 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-006-353A-7

Query Match 100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
|||||
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
|||||
Qy 61 KPCPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHLEVEINCT 120
|||||
Db 61 KPCPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHLEVEINCT 120
|||||
Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
|||||
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
|||||
Qy 181 LLPIPLIYVWKRKEVQKTCRKHRKENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
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Db 181 LLPIPLIYVWKRKEVQKTCRKHRKENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
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Qy 241 TILSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
|||||
Db 241 TILSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
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Qy 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335

Db 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335
|||||
RESULT 5
US-08-468-560C-2
: Sequence 2, Application US/08468560C
: Patent No. 6270998
: GENERAL INFORMATION:
: APPLICANT: NAGATA, Shigekazu
: APPLICANT: ITOH, Naoto
: APPLICANT: YONEHARA, Shin
: TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
: TITLE OF INVENTION: ANTIGEN
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
: STREET: P.O. BOX 747
: CITY: FALLS CHURCH
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,560C
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: MURPHY JR., GERLAD M.
: REGISTRATION NUMBER: 28,977
: REFERENCE/DOCKET NUMBER: 20-4393P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-205-8000
: TELEFAX: 703-205-8050
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 335 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-468-560C-2

Query Match 100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
|||||
Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
|||||
Qy 61 KPCPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHLEVEINCT 120
|||||
Db 61 KPCPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLCDGEGHLEVEINCT 120
|||||
Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
|||||
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
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Qy 181 LLPIPLIYVWKRKEVQKTCRKHRKENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
|||||
Db 181 LLPIPLIYVWKRKEVQKTCRKHRKENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
|||||
Qy 241 TILSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
|||||
Db 241 TILSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
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Qy 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335
|||||
Db 301 ANLCTLAEKIQTIIILKDTSDSENSFRNEIQSLV 335

```
RESULT 6
US-09-180-100-20
; Sequence 20, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-20

Query Match      100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCNSTVCEHCDPCTKCEHGIIECTLTNTKCEGSRSLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCNSTVCEHCDPCTKCEHGIIECTLTNTKCEGSRSLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

RESULT 7
US-09-565-918-3
; Sequence 3, Application US/09565918.
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722

Query Match      100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCNSTVCEHCDPCTKCEHGIIECTLTNTKCEGSRSLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCNSTVCEHCDPCTKCEHGIIECTLTNTKCEGSRSLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

RESULT 8
US-09-573-986-7
; Sequence 7, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-7

Query Match      100.0%; Score 1804; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSLVARLSSKSVNAQVTDINSKGLRLKRTVTTVETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCRLCDGEGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFNCNSTVCEHCDPCTKCEHGIIECTLTNTKCEGSRSLGWLCLL 180
Db 121 RTQNTKCRCKPNFNCNSTVCEHCDPCTKCEHGIIECTLTNTKCEGSRSLGWLCLL 180
QY 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIYVWKRKEVQKTCRKRKENOGSHESPTLNPETVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
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Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
QY 181 LLPIPLVWVKREVKQTKCRKHENOGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLVWVKREVKQTKCRKHENOGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335

RESULT 9
PCT-US95-17083-2
; Sequence 2, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; FILING DATE: PCT/US95/17083
; PRIOR APPLICATION NUMBER: US95-17083
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17083-2

Query Match 100.0%; Score 1804; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
QY 181 LLPIPLVWVKREVKQTKCRKHENOGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLVWVKREVKQTKCRKHENOGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335

RESULT 10
US-09-013-895A-3
; Sequence 3, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.

; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 5410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,895A
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 669 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-895A-3

Query Match 100.0%; Score 1804; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 4.1e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
Db 121 RTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGIKECTLTSTNTKCKEGRSRLNGLWCLL 180
QY 181 LLPIPLVWVKREVKQTKCRKHENOGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLVWVKREVKQTKCRKHENOGSHESPTLPETVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGfVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQHLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIOSLV 335

RESULT 11
US-09-448-868-3
; Sequence 3, Application US/09448868
; Patent No. 6461923
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian

APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-868-3

Query Match 100.0%; Score 1804; DB 4; Length 669;
Best Local Similarity 100.0%; Pred. No. 4.1e-160;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKKEGSRNLGWLCLL 180
QY 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQGSHPETLNPETVAINLSVDLSKYITTAGVM 240
Db 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQGSHPETLNPETVAINLSVDLSKYITTAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHLGKKEAYDFLIKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHLGKKEAYDFLIKDLKK 300
QY 301 ANLCTLAETQITILKIDTSSENSFRNEIQSLV 335
Db 301 ANLCTLAETQITILKIDTSSENSFRNEIQSLV 335

RESULT 12
US-08-815-469-6
Sequence 6, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-6

Query Match 99.3%; Score 1792; DB 4; Length 335;
Best Local Similarity 99.7%; Pred. No. 2.1e-159;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
Db 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTETONLEGLHHDGQFCH 60
QY 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
Db 61 KCPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKKEGSRNLGWLCLL 180
Db 121 RTQNTKCRCKPNFCNSTVCEHCDPCTKCEHGIKECTLTSTNTKKEGSRNLGWLCLL 180
QY 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQGSHPETLNPETVAINLSVDLSKYITTAGVM 240
Db 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQGSHPETLNPETVAINLSVDLSKYITTAGVM 240

Qy 241 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNNHQLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNNHQLHGKKEAYDTLIKDLKK 300
Qy 301 ANLCTLAEKIOTIILKIDTSDSENSFRNEIOSLV 335
Db 301 ANLCTLAEKIOTIILKIDTSDSENSFRNEIOSLV 335

RESULT 13
US-09-086-483A-3
; Sequence 3, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-3

Query Match 96.68; Score 1743; DB 4; Length 331;
Best Local Similarity 98.88; Pred. No. 7.6e-155;
Matches 331; Conservative 0; Mismatches 0; Indels 4; Gaps 4;
Qy 1 MGLIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MGLIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 59
Qy 61 KPCPPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLEYEINCT 120
Db 60 -PCPPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLEYEINCT 118
Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKCTLTNTKCKEGRSRLGWLCCL 180
Db 119 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKCTLTNTKCKEGRSRLGWLCCL 177

Qy 181 LLPIPLIWMVRKEVQKTCRKHRENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 240
Db 178 LLPIPLIWMVRKEVQKTCRKHRENQGSHPSTLNPTVAINLSDVLSKYITTIAGVM 237
Qy 241 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNNHQLHGKKEAYDTLIKDLKK 300
Db 238 TLSQVKGVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNNHQLHGKKEAYDTLIKDLKK 297
Qy 301 ANLCTLAEKIOTIILKIDTSDSENSFRNEIOSLV 335
Db 298 ANLCTLAEKIOTIILKIDTSDSENSFRNEIOSLV 331

RESULT 14
US-08-444-231-19
; Sequence 19, Application US/08444231
; Patent No. 5652210
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIERER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/152,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-231-19

Query Match 92.4%; Score 1667.5; DB 1; Length 314;
Best Local Similarity 93.7%; Pred. No. 8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
Qy 1 MGLIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Db 1 MGLIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLLELRKTVTTVETQNLGLHHDGQFCH 60
Qy 61 KPCPPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLEYEINCT 120
Db 61 KPCPPGGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDCDGHGLEYEINCT 120
Qy 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKCTLTNTKCKEGRSRLGWLCCL 180

Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLSNTKCEE----- 168
QY 181 LLPIPLIIVWVRKKEVQKTCRKHKENQGSHPETLNPEVAINLSDVLSKYITTIAGVM 240
Db 169 -----VKRKEVQKTCRKHKENQGSHPETLNPEVAINLSDVLSKYITTIAGVM 219
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 279
QY 301 ANLCTLAEKIQTIIILKDTSDSENSFNFRNEIOSLV 335
Db 280 ANLCTLAEKIQTIIILKDTSDSENSFNFRNEIOSLV 314

RESULT 15

US-08-152-443A-19
; Sequence 19, Application US/08152443A
; Patent No. 5663070
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,443A
; FILING DATE: 15-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-152-443A-19

Query Match 92.4%; Score 1667.5; DB 1; Length 314;
Best Local Similarity 93.7%; Pred. No. 8e-148; 0; Mismatches 0; Indels 21; Gaps 1;
Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTTVTQNLGLHHDGQFCH 60
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDVCPQEGKEYTDKAHFSSKRCRLCDEGHGLEVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDVCPQEGKEYTDKAHFSSKRCRLCDEGHGLEVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLSNTKCEE----- 168
Db 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLSNTKCEE----- 168

QY 181 LLPIPLIIVWVRKKEVQKTCRKHKENQGSHPETLNPEVAINLSDVLSKYITTIAGVM 240
Db 169 -----VKRKEVQKTCRKHKENQGSHPETLNPEVAINLSDVLSKYITTIAGVM 219
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 300
Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKQVLLRNHQLHGKKEAYDTLIKDLKK 279
QY 301 ANLCTLAEKIQTIIILKDTSDSENSFNFRNEIOSLV 335
Db 280 ANLCTLAEKIQTIIILKDTSDSENSFNFRNEIOSLV 314

Search completed: May 9, 2003, 17:08:24
Job time : 15.1571 secs

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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:05:23 ; Search time 16.6994 Seconds
(without alignments)
1846.092 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MGIWTLPLVLTSLVARLSS.....KDTSDSENFRNIQISLV 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	100.0	335	10	US-09-826-212-7
2	1804	100.0	335	10	US-09-802-669-2
3	1804	100.0	335	10	US-09-949-713-20
4	1804	100.0	335	10	US-09-874-138-4
5	1804	100.0	335	10	US-09-884-987-2
6	1804	100.0	335	10	US-09-935-727-9
7	1804	100.0	335	12	US-10-005-842-4
8	1804	100.0	669	9	US-10-226-296-3
9	1804	100.0	669	9	US-10-226-318-3
10	1792	99.3	335	9	US-09-314-889-6
11	1792	99.3	335	10	US-09-333-966-6
12	1484	82.3	281	9	US-09-756-854-3
13	1484	82.3	281	9	US-10-041-574-3
14	997	55.3	237	9	US-09-925-299-960
15	997	55.3	237	10	US-09-925-299-960
16	942	52.2	167	9	US-10-112-793-22
17	893	49.5	157	10	US-09-949-713-15
18	856	47.5	327	10	US-09-802-669-66
19	811.5	45.0	144	10	US-09-949-713-21

20	811.5	45.0	159	10	US-09-949-713-23	Sequence 23, Appl
21	811.5	45.0	376	10	US-09-949-713-22	Sequence 22, Appl
22	757	42.0	128	10	US-09-949-713-9	Sequence 9, Appl
23	757	42.0	143	10	US-09-949-713-10	Sequence 10, Appl
24	757	42.0	360	10	US-09-949-713-11	Sequence 11, Appl
25	712	39.5	119	9	US-10-112-793-15	Sequence 15, Appl
26	712	39.5	119	10	US-09-800-909-5	Sequence 5, Appl
27	712	39.5	119	10	US-09-884-987-3	Sequence 3, Appl
28	712	39.5	119	10	US-09-800-908-14	Sequence 14, Appl
29	579.5	32.1	204	10	US-09-948-018-18	Sequence 18, Appl
30	393	21.8	77	9	US-10-112-793-24	Sequence 24, Appl
31	386	21.4	77	9	US-09-992-964-17	Sequence 17, Appl
32	386	21.4	77	10	US-09-887-879-17	Sequence 17, Appl
33	352	19.5	68	9	US-09-756-854-22	Sequence 22, Appl
34	352	19.5	68	9	US-10-041-574-22	Sequence 22, Appl
35	328	18.2	63	12	US-10-035-408-1	Sequence 1, Appl
36	206	11.4	283	10	US-09-924-231-2	Sequence 2, Appl
37	206	11.4	283	10	US-09-934-289A-13	Sequence 13, Appl
38	206	11.4	283	10	US-09-935-727-31	Sequence 31, Appl
39	206	11.4	283	12	US-10-020-787-2	Sequence 2, Appl
40	206	11.4	283	12	US-10-066-209-2	Sequence 2, Appl
41	206	11.4	833	9	US-10-226-296-5	Sequence 5, Appl
42	206	11.4	833	9	US-10-226-318-5	Sequence 5, Appl
43	205.5	11.4	350	9	US-10-076-754-6	Sequence 6, Appl
44	205.5	11.4	350	9	US-10-076-773-6	Sequence 6, Appl
45	205.5	11.4	350	12	US-10-067-615-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-826-212-7
; Sequence 7, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; APPLICANT: NI, Jian
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280006
; CURRENT APPLICATION NUMBER: US/09/826.212
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-7

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGIWTLPLVLTSLVARLSSVNAQVTDINSKGLRLKRTVTETQNLGLHHDGQFCH	60
DB	1	MGIWTLPLVLTSLVARLSSVNAQVTDINSKGLRLKRTVTETQNLGLHHDGQFCH	60
QY	61	KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT	120
DB	61	KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRCDEGHGVEINCT	120
QY	121	RTQNTKRCCKPNFNCSTVCEHCDPCTKCEHGIKECTPLTNTKCKEGSRNLGWLCLL	180
DB	121	RTQNTKRCCKPNFNCSTVCEHCDPCTKCEHGIKECTPLTNTKCKEGSRNLGWLCLL	180
QY	181	LLPIPLIWWKRKEVQKTCRKHKRKNQGSHPINLPETVAINLSDVDLSKIYITTIAGVM	240
DB	181	LLPIPLIWWKRKEVQKTCRKHKRKNQGSHPINLPETVAINLSDVDLSKIYITTIAGVM	240
QY	241	TLSQVKGVKRVNGVNEAKIDEIKNDVQDTAEQVOLLRNHQLHGKKEAYDTLLIKLKK	300

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|||||
Db 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTILKDTSDSENSFRNEIQSLV 335
|||||
Db 301 ANLCTLAETKIQTILKDTSDSENSFRNEIQSLV 335

RESULT 2
US-09-802-669-2
; Sequence 2, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-669-2

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLELRKVTVTETONLGLHHGQFCH 60
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLELRKVTVTETONLGLHHGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVVVKRKEVQKTCRKRKENGSGHESPTLPETVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIVVVKRKEVQKTCRKRKENGSGHESPTLPETVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETKIQTILKDTSDSENSFRNEIQSLV 335

RESULT 3
US-09-949-713-20
; Sequence 20, Application US/09949713
; Patent No. US20020044944A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. US20020044944A1
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
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; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-20

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLELRKVTVTETONLGLHHGQFCH 60
Db 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLELRKVTVTETONLGLHHGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDEGHGVEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEGRSRLGWLCLL 180
Db 121 RTQNTKCRCKPNEFCNSTVCEHCDPCTKCEHGIKECTLTSTNCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVVVKRKEVQKTCRKRKENGSGHESPTLPETVAIINLSDVDLSKYITTIAGVM 240
Db 181 LLPIPLIVVVKRKEVQKTCRKRKENGSGHESPTLPETVAIINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
Db 241 TLSQVGFVRKNGVNEAKIDEIKNDVQDTAEQKVQLLRNHWLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETKIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETKIQTILKDTSDSENSFRNEIQSLV 335

RESULT 4
US-09-874-138-4
; Sequence 4, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 335
; TYPE: PRT
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ORGANISM: Homo sapiens
US-09-874-138-4

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGFCH 60
DB 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGFCH 60
QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
DB 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
QY 181 LPIPLIIVWVKRKEVQTKRKHREKQSGHESPTLNPEVAINLSVDLSKYITTIAGVM 240
DB 181 LPIPLIIVWVKRKEVQTKRKHREKQSGHESPTLNPEVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335

RESULT 5

US-09-884-987-2
Sequence 2, Application US/09884987
Patent No. US20020102653A1
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu et al
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-987-2

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGFCH 60
DB 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGFCH 60
QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
DB 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
QY 181 LPIPLIIVWVKRKEVQTKRKHREKQSGHESPTLNPEVAINLSVDLSKYITTIAGVM 240
DB 181 LPIPLIIVWVKRKEVQTKRKHREKQSGHESPTLNPEVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300

QY 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335
DB 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335

RESULT 6

US-09-935-727-9
Sequence 9, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-727-9

Query Match 100.0%; Score 1804; DB 10; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGFCH 60
DB 1 MGIWTLPLVLSVARLSKSNVAQVTDINSKGLRLKTVTTVETQNLGLHHDGFCH 60
QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
DB 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLCDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
DB 121 RTQNTKCRCKPNFPCNSTVCEHCDPCTKCEHGIIECTLTSTNTKCEGSRNLGLCLL 180
QY 181 LPIPLIIVWVKRKEVQTKRKHREKQSGHESPTLNPEVAINLSVDLSKYITTIAGVM 240
DB 181 LPIPLIIVWVKRKEVQTKRKHREKQSGHESPTLNPEVAINLSVDLSKYITTIAGVM 240
QY 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVGFVRKNGVNEAKIDEIKNDNVQDTAEQVOLLRNHOLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIOTILKDTSDSENSNFRNEIQSLV 335

Db 301 ANLCTLAEKIQIILKDTSDSENSFRNEIOSLV 335
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RESULT 7

US-10-005-842-4

; Sequence 4, Application US/10005842

; Patent No. US20020098550A1

; GENERAL INFORMATION:

; APPLICANT: NI, Jian

; Gentz, Reiner

; Yu, Guo-Liang

; Su, Jeffrey

; Rosen, Craig A.

; TITLE OF INVENTION: Death Domain Containing Receptor 5

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/005,842

; FILING DATE: 07-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/042,583

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 60/040,846

; FILING DATE: 17-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hoover, Kenley

; REGISTRATION NUMBER: 40,302

; REFERENCE/DOCKET NUMBER: PF366

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 3013098504

; TELEFAX: 3013098439

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 335 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-005-842-4

Query Match 100.0%; Score 1804; DB 12; Length 335;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDGEGHGLEVEINCT 120

Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDGEGHGLEVEINCT 120

QY 121 RTQNTKCRCKNFNCSNVCCHCDPCTKCEHGIIECTLTNTKCKEGSRNLGWLCLL 180

Db 121 RTQNTKCRCKNFNCSNVCCHCDPCTKCEHGIIECTLTNTKCKEGSRNLGWLCLL 180

QY 181 LLPIPLIIVWKRKEVQKTCRKHRENOGSHESPTLNPTVAINLSDVDLSKIYITTIAGVM 240

Db 181 LLPIPLIIVWKRKEVQKTCRKHRENOGSHESPTLNPTVAINLSDVDLSKIYITTIAGVM 240

QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKOLLRNWHLHGKKEAYDTLIKDLKK 300
|||||
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKOLLRNWHLHGKKEAYDTLIKDLKK 300
|||||
QY 301 ANLCTLAEKIQIILKDTSDSENSFRNEIOSLV 335
|||||
Db 301 ANLCTLAEKIQIILKDTSDSENSFRNEIOSLV 335
|||||

RESULT 8

US-10-226-296-3

; Sequence 3, Application US/10226296

; Publication No. US20030036168A1

; GENERAL INFORMATION:

; APPLICANT: NI, Jian

; Rosen, Craig A.

; Pan, James G. L.

; Gentz, Reiner L.

; Dixit, Vishva M.

; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
Receptor 4), Member of the TNF-Receptor
Superfamily and Binding to Trail (AP02-L)

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/226,296

; FILING DATE: 23-Aug-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/448,868

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 09/013,895

; FILING DATE: 27-JAN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.13000004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 669 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-226-296-3

Query Match

100.0%; Score 1804; DB 9; Length 669;

Best Local Similarity 100.0%; Pred. No. 2.3e-130;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60

Db 1 MLGIWTLPLVLTSLVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDGEGHGLEVEINCT 120

Db 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCRLCDGEGHGLEVEINCT 120

QY 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIWWKRKEVQKTCRKHRKENGSHESPTLNPTVAINLSVDLSKYIITTIAGVM 240
DB 181 LLPIPLIWWKRKEVQKTCRKHRKENGSHESPTLNPTVAINLSVDLSKYIITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIOTIILKDTSDSENSFRNEIQSLV 335
DB 301 ANLCTLAETIOTIILKDTSDSENSFRNEIQSLV 335

RESULT 9

US-10-226-318-3
; Sequence 3, Application US/10226318
; Publication No. US20030073187A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Rosen, Craig A.
; Pan, James G.
; Gentz, Reiner L.
; Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
; Receptor 4), Member of the TNF-Receptor
; Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/226,318

FILING DATE: 23-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/448,868

FILING DATE: <Unknown>

APPLICATION NUMBER: 09/013,895

FILING DATE: 27-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1300004

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 669 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-226-318-3

Query Match 100.0%; Score 1804; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 2.3e-130;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLGLRKTVTTVETONLEGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLGLRKTVTTVETONLEGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLCDEGHGLEYEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRCLCDEGHGLEYEINCT 120
QY 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRKPNFNCSTVCEHCDPCTKCEHGIIECTLTSTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIWWKRKEVQKTCRKHRKENGSHESPTLNPTVAINLSVDLSKYIITTIAGVM 240
DB 181 LLPIPLIWWKRKEVQKTCRKHRKENGSHESPTLNPTVAINLSVDLSKYIITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAETIOTIILKDTSDSENSFRNEIQSLV 335
DB 301 ANLCTLAETIOTIILKDTSDSENSFRNEIQSLV 335

RESULT 10

US-09-314-889-6
; Sequence 6, Application US/09314889
; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P. L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/314,889

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/815,469

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,711

FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 335 amino acids

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; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-09-314-889-6

Query Match
Best Local Similarity 99.3%; Score 1792; DB 9; Length 335;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVTQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDDEGHGVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVWVKRKEVQKTCRKHKENQGSHPSTLNPETVAINLSDVDLSKYITTIAGVM 240
DB 181 LLPIPLIVWVKRKEVQKTCRKHKENQGSHPSTLNPETVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIQTIIKIDITSSENSNFRNEIQSLV 335
DB 301 ANLCTLAEKIQTIIKIDITSSENSNFRNEIQSLV 335

RESULT 11
US-09-333-966-6
; Sequence 6, Application US/09333966
; Patent No. US20020009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285

```

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; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20020009773A1 Relevant
; TOPOLOGY: No. US20020009773A1 Relevant
; MOLECULE TYPE: protein
US-09-333-966-6

Query Match
Best Local Similarity 99.3%; Score 1792; DB 10; Length 335;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVTQNLGLHHDGQFCH 60
DB 1 MGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKTVTVTQNLGLHHDGQFCH 60
QY 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDDEGHGVEINCT 120
DB 61 KPCPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHFSKRCRCLDDEGHGVEINCT 120
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGWLCLL 180
DB 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTLTNTKCKEGRSRLGWLCLL 180
QY 181 LLPIPLIVWVKRKEVQKTCRKHKENQGSHPSTLNPETVAINLSDVDLSKYITTIAGVM 240
DB 181 LLPIPLIVWVKRKEVQKTCRKHKENQGSHPSTLNPETVAINLSDVDLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
DB 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHQLHGKKEAYDTLIKDLKK 300
QY 301 ANLCTLAEKIQTIIKIDITSSENSNFRNEIQSLV 335
DB 301 ANLCTLAEKIQTIIKIDITSSENSNFRNEIQSLV 335

RESULT 12
US-09-756-854-3
; Sequence 3, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Human Tumor Necrosis Factor Receptor TR9
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>

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Query Match 55.3%; Score 997; DB 9; Length 237;
 Best Local Similarity 96.8%; Pred. No. 4.7e-69;
 Matches 179; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
 DB 53 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 112

QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDEGHGLXVEINCT 120
 DB 113 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDEGHGLXVEINCT 172

QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTILTSNTKCKEGRSRLGWLCLL 180
 DB 173 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTILTSNTKCKEGRSRLGWLCLL 232

QY 181 LLPIP 185
 DB 233 LLPIP 237

Search completed: May 9, 2003, 17:09:07
 Job time : 20.6994 secs

RESULT 15
 US-09-925-299-960
 ; Sequence 960, Application US/09925299
 ; Patent No. US20020055627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA102
 ; CURRENT APPLICATION NUMBER: US/09/925,299
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05883
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 960
 ; LENGTH: 237
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (68)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (166)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (177)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (187)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (223)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-925-299-960

Query Match 55.3%; Score 997; DB 10; Length 237;
 Best Local Similarity 96.8%; Pred. No. 4.7e-69;
 Matches 179; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 60
 DB 53 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLRLKRTVTVTQNLGLHHDGQFCH 112

QY 61 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDEGHGLXVEINCT 120
 DB 113 KCPGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKRCRCLDCDEGHGLXVEINCT 172

QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIECTILTSNTKCKEGRSRLGWLCLL 180

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 17:02:31 ; Search time 28.8444 seconds
(without alignments)
1116.509 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804

Sequence: 1 MGIWTLPLVLTSVARLSS.....KDIITSDSENFRNIQSLV 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1804	100.0	335	2	A40036	apoptosis-mediating
2	1667.5	92.4	314	2	I37383	FAS soluble protei
3	856	47.5	327	2	A46484	apoptosis-mediati
4	827.5	45.9	324	2	JC2395	Fas antigen precu
5	621.5	34.5	149	2	S58662	Fas-Delta-(4,7) pr
6	342.5	19.0	103	2	I37384	FAS soluble protei
7	185.5	10.3	435	2	I54182	tumor necrosis fac
8	182	10.1	416	1	JN0006	nerve growth facto
9	177	9.8	455	1	GQHUT1	tumor necrosis fac
10	173.5	9.6	305	2	A46476	B cell-associated
11	164.5	9.1	250	1	A49053	CD27 antigen precu
12	161.5	9.0	277	2	A60771	B-cell activation
13	161	8.9	461	2	JC4302	tumor necrosis fac
14	159.5	8.8	260	1	A46517	CD27 antigen precu
15	159	8.8	427	1	GQHUN	nerve growth facto
16	156	8.6	425	1	A26431	nerve growth facto
17	146	8.1	454	1	GQMST1	tumor necrosis fac
18	144	8.0	272	2	I48700	gene ox40 protein
19	141.5	7.8	271	2	S12783	ox40 antigen precu
20	141.5	7.8	461	1	A35356	tumor necrosis fac
21	141	7.8	349	2	D72175	G2R protein - vari
22	139	7.7	348	2	T28623	hypothetical prote
23	139	7.7	349	2	D36858	gene G4R protein -
24	136.5	7.6	383	2	S53716	delta-like homeoti
25	131.5	7.3	385	2	A54785	preadipocyte facto
26	131.5	7.3	2180	2	T29764	hypothetical prote
27	130.5	7.2	677	2	C42125	trophozoite cystei
28	129.5	7.2	326	1	GQVZML	T2 protein - myxom
29	129.5	7.2	385	2	S53718	homeotic protein d

30 128 7.1 728 2 I50719 C-Delta-1 - chicke
31 125.5 7.0 574 2 B88465 protein B0244.8 [i
32 125 6.9 1014 2 T30545 major surface glyco
33 124.5 6.9 325 2 B43692 T2 protein - rabbi
34 122.5 6.8 461 1 GQRTT1 tumor necrosis fac
35 121.5 6.7 474 2 B38634 tumor necrosis fac
36 121.5 6.7 1766 2 A42125 trophozoite cystei
37 120.5 6.7 277 2 I37552 OX40 homolog - hum
38 120.5 6.7 459 2 I48854 gene murine tumour
39 119.5 6.6 1274 2 T42017 cysteine rich prot
40 119 6.6 577 2 A60501 thrombomodulin pre
41 118.5 6.6 1786 1 MMHUB1 laminin beta-1 cha
42 117.5 6.5 1111 2 T26972 hypothetical prote
43 115.5 6.4 1372 2 T25933 hypothetical prote
44 115 6.4 1104 2 I38869 transcription fact
45 114.5 6.3 1816 1 S68960 laminin alpha-4 ch

ALIGNMENTS

RESULT 1

A40036

apoptosis-mediating surface antigen Fas precursor - human

N:Alternate names: surface antigen APO-1

C:Species: Homo sapiens (man)

C>Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000

C:Accession: A40036; S24543; A38142

R:Itch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.;

Cell 66, 233-243, 1991

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <ITD>

A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R:Krammer, P.H.

submitted to the EMBL Data Library, February 1992

A:Reference number: S24543

A:Accession: S24543

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <KRA>

A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Mair, G.; Klas, C.; Li-Weber, M.;

J. Biol. Chem. 267, 10709-10715, 1992

A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a mem

A:Reference number: A38142; MUID:92268122; PMID:1375228

A:Accession: A38142

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-134, 'Q', 136-335 <OEH>

A:Experimental source: SKW6.4 cells

A>Note: sequence extracted from NCBI backbone (NCBIP:103810)

A>Note: in NCBI backbone the source is designated as mouse

C:Genetics:

A:Gene: GDB:APR1

A:Cross-references: GDB:132671; OMIM:134637

A:Map position: 10q24.1-10q24.1

C:Superfamily: NGF receptor repeat homology

C:Keywords: apoptosis; surface antigen; transmembrane protein

F:1-16/Domain: signal sequence #status predicted <SIG>

F:85-128/Domain: NGF receptor repeat homology <NG4>

F:174-190/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 100.0%; Score 1804; DB 2; Length 335;

Matches 335; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRKTVTVTQNLGLHHDQFCH 60

Db 1 MGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLRKTVTVTQNLGLHHDQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPDCVQCEGKEYTDKAHFSKRCRCRLCDEGHGLEYEINCT 120
Db 61 KPCPPGERKARDCTVNGDEPDCVQCEGKEYTDKAHFSKRCRCRLCDEGHGLEYEINCT 120
QY 121 RTQNTKCRCKPNFNVSTVCEHCDPCTKCEHGIIKECTLTSTNTKCKEGRSRLNLGWLCLL 180
Db 121 RTQNTKCRCKPNFNVSTVCEHCDPCTKCEHGIIKECTLTSTNTKCKEGRSRLNLGWLCLL 180
QY 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQSHESPTLNPTVAINLSDVLSKYITTIAGVM 240
Db 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQSHESPTLNPTVAINLSDVLSKYITTIAGVM 240
QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHOLHGKKEAYDTLTKDLKK 300
Db 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHOLHGKKEAYDTLTKDLKK 300
QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335
Db 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

RESULT 2

I37383

FAS soluble protein - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C:Accession: I37383

R:Cascino, I.; Flucci, G.; Papoff, G.; Ruberti, G.

J. Immunol. 154, 2706-2713, 1995

A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A:Reference number: I37383; MUID:95181785; PMID:7533181

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-314 <RES>

A:Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539

Query Match

Best Local Similarity 92.4%; Score 1667.5; DB 2; Length 314;

Matches 314; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 MGLTWTLLPLVLTLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60

Db 1 MGLTWTLLPLVLTLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPDCVQCEGKEYTDKAHFSKRCRCRLCDEGHGLEYEINCT 120

Db 61 KPCPPGERKARDCTVNGDEPDCVQCEGKEYTDKAHFSKRCRCRLCDEGHGLEYEINCT 120

QY 121 RTQNTKCRCKPNFNVSTVCEHCDPCTKCEHGIIKECTLTSTNTKCKEGRSRLNLGWLCLL 180

Db 121 RTQNTKCRCKPNFNVSTVCEHCDPCTKCEHGIIKECTLTSTNTKCKEGRSRLNLGWLCLL 180

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Db 169 -----VVRKEVQKTCRKHKENQSHESPTLNPTVAINLSDVLSKYITTIAGVM 219

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Db 220 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHOLHGKKEAYDTLTKDLKK 279

QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

Db 280 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 314

QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 335

Db 280 ANLCTLAETIQTILKDTSDSENSFRNEIQSLV 314

RESULT 3

A46484

apoptosis-mediating membrane-associated polypeptide Fas - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: A46484; A47254

R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jen, J. Immunol. 148, 1274-1279, 1992
A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas
A:Reference number: A46484; MUID:92148151; PMID:1371136
A:Accession: A46484

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-327 <WAT>

A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226

A:Experimental source: BAM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)

R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993

A:Title: Aberrant transcription caused by the insertion of an early transposable element
A:Reference number: A47254; MUID:93189576; PMID:7680478
A:Accession: A47254

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <ADA>

A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506

A:Experimental source: MRL lpr/lpr

A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126853)

C:Superfamily: NGF receptor repeat homology

C:Keywords: transmembrane protein

F:44-79/Domain: NGF receptor repeat homology <NGF>

F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match

Best Local Similarity 47.5%; Score 856; DB 2; Length 327;

Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MGLTWTLLPLVLTLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60

Db 1 MGLTWTLLPLVLTLSVARLSKSVNAQVTDINSKGLERKVTVTETQNLGLHHDGQFCH 60

QY 61 KPCPPGERKARDCTVNGDEPDCVQCEGKEYTDKAHFSKRCRCRLCDEGHGLEYEINCT 120

Db 57 QPCPGKKVDECKMNGGTTCAPCTEGKEYMDKNHVDKRCCTCLCDEGHGLEYEINCT 116

QY 121 RTQNTKCRCKPNFNVSTVCEHCDPCTKCEHGIIKECTLTSTNTKCKEGRSRLNLGWLCLL 180

Db 117 LTQNTKCRCKPNFNVSTVCEHCDPCTKCEHGIIKECTLTSTNTKCKEGRSRLNLGWLCLL 176

QY 181 LLPIPLIPLVWVKRKEVQKTCRKHKENQSHESPTLNPTVAINLSDVLSKYITTIAGVM 240

Db 177 VLLIPL-VFIYRKYRKKWKRRQDDP---ESRTSSRETIPMNASLSKYIPRIAEEM 232

QY 241 TLSQVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHOLHGKKEAYDTLTKDLKK 300

Db 233 TIQEAKKFARENNIKSGKIDIMHDSIQDTAEQKVOLLRWYSHGKSDAYQDLIKGLKK 292

QY 301 ANLCTLAETIQTILKDTSDSENSFRNEIQSL 334

Db 293 ACERLTDRFQDMVQKDLGKSTPDTGNEBQCL 326

RESULT 4

JC2395

Fas antigen precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C:Accession: JC2395; PC2246

R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.

Biochem. Biophys. Res. Commun. 198, 666-674, 1994

A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat
A:Reference number: JC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395

A:Molecule type: mRNA

A:Residues: 1-324 <KIM>

A:Cross-references: DBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g4684

A:Experimental source: thymus

A:Accession: PC2246

A:Molecule type: mRNA

C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
E:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) #status predicted

Query Match 9.0%; Score 161.5; DB 2; Length 277;
Best Local Similarity 26.3%; Pred. No. 0.00042;
Matches 66; Conservative 31; Mismatches 89; Indels 65; Gaps 14;

QY 59 CHKPCPPGKARCDVTNGDEPCVPCQEGKEYTDKAHFSKRCRCLDGHGLEVEIN 118
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
37 CCSLCQGQKLVSCT-EFTETELCPGE-SFELDTWNRETHQHQRICDPNLGLRVQQK 94
QY 119 CTRTQNTKCRKPFFCNSTVCHECDPCKCEHG-IKE-CITLSTNFKCK--EEGSRSNL 174
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
95 GTSETDAICTICEGWCHCTSEACSVLRSCSPGFVKQIATGVSDTICEPCPVGGFFSNV 154
QY 175 G-----W-----LC-----LLLLPI-----PLIVVWK 191
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
155 SSAFEKHPWTSCETKDVLVVOAGTKNTDVCGPDRLRALVWIPIIFILFAILLLVLF 214
QY 192 RKEYQKTCRKHKRENQCESHESPTLNPETVAINLSVDVLSKVIT-----TIAGVMTLSOV 245
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
215 IKKVAK----KPTNKAPH--PKPEQP--EINFPD-DLPGSNTAAPVOEILHCQPVITQE 264
QY 246 KGFVRKNQNVNE 256
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
265 DGRESISVQOE 275

RESULT 13
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor
A:Reference number: JC4302; UID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUM>
A:Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NGI>
F:84-126/Domain: NGF receptor repeat homology <NGI>
F:211-231/Domain: transmembrane #status predicted <TM>
F:361-447/Domain: signal transduction #status predicted <SIT>
F:54,145,151/Binding site: carbohydrate (Asn) #status predicted

Query Match 8.9%; Score 161; DB 2; Length 461;
Best Local Similarity 18.6%; Pred. No. 0.00076;
Matches 86; Conservative 45; Mismatches 147; Indels 184; Gaps 15;

QY 7 LLPLVLTSSVARLSSSVNAQVTDINSKGLRLKKTVTTVETQNLGLHHDGQFCH----- 60
D 10 LLPLVL-----RALLVDVYPAGVGLVHPG-----DREKRSLCPQGGKYSHPQNRSI 57
QY 61 --KPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFS-----SKCR----- 102
D 58 CCKTKHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTCLSCSKCRSEMSQVEISPC 117
QY 103 -----RCRLCDEGHGLEVEINCRTONTKCRCKPNEFC 135
D 118 TVDRTVGCRKNQYRKWTSETFLFCLNCLCPNG---TVQLPCLKEODTICNCHSGFEL 174
QY 136 NSTVCEHCDPCTKCBGHIKE-CTLTSNTKCKEGRSRLGLWLLPILPLVWV----- 190
D 175 RD---KECVSCVCKNADCKNLCPATSETR-----NDFQDTGTVLL-----PLVIFGLCL 223
QY 191 -----KREVKQTCRKHRENQGSHE----- 211
D 224 AFFLEVGLACRYQRWKPKLYSLICGKSTPVKEGEPEPLATAPSGPITTFSPISFPTT 283
QY 212 -----SPTLNP----- 217
D 284 TSPVPSPSPSTSPFTTCDHNSNIKVTSPPKELAPPQAGPILPMPASTPVPPLPKW 343
QY 218 -----ETVAINLSVDLSKYITTIAGVMTLSQVKGVRKNGVNEAKIDEIKNDNVQDT 270
D 344 GGSAAHSASAPALADAPATLYAVVDGVP-TRNKEFVRRLGLEHEIERLELQNGRL 402
QY 271 AEQVQLLRNHHQHGKEA-YDTLIKDLKKNALCTLAQIK 311
D 403 REAQYSLAEWRRRTSRREATLELGLSVLRMDLLGLCLEDIE 444

RESULT 14

A46517
CD27 antigen precursor - human
N:Alternate names: CD27L receptor; T cell activation antigen CD27
C:Species: Homo sapiens (man)
C:Date: 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
A:Accession: A46517; A46454
R:Loenen, W.A.; Gravestien, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J. J. Immunol. 149, 3937-3943, 1992
A:Title: Genomic organization and chromosomal localization of the human CD27 gene.
A:Reference number: A46517; MUID:93094588; PMID:1334106
A:Accession: A46517
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-260 <LOE>
A:Note: sequence extracted from NCBI backbone (NCBIP:120386)
R:Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B. J. Immunol. 147, 3165-3169, 1991
A:Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumor necrosis factor receptor superfamily.
A:Reference number: A46454; MUID:92013149; PMID:1655907
A:Accession: A46454
A:Molecule type: mRNA
A:Residues: 1-58, 'A', 'G', '60-260 <CAM>
A:Cross-references: GB:M63928; NID:g180084; PIDN:AAA58411.1; PID:g180085
A:Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBIP:60289)
C:Comment: A soluble CD27 found in serum and urine is formed by proteolysis.
C:Genetics:
A:Gene: GDB:CD27
A:Cross-references: GDB:132582; OMIM:186711
A:Map position: 12p13-12p13
A:Introns: 46/1; 90/1; 150/1; 180/1; 220/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface antigen
F:1-260/Domain: signal sequence #status predicted <SIG>
F:21-260/Product: CD27 antigen #status predicted <MAT>
F:21-191/Domain: extracellular #status predicted <EXT>
F:27-63/Domain: NGF receptor repeat homology <NG1>
F:65-105/Domain: NGF receptor repeat homology <NG2>
F:121-186/Region: proline/serine/threonine-rich

F:192-211/Domain: transmembrane #status predicted <TMN>
F:212-260/Domain: intracellular #status predicted <INT>
F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 8.8%; Score 159.5; DB 1; Length 260;
Best Local Similarity 34.4%; Pred. No. 0.00055;
Matches 31; Conservative 10; Mismatches 46; Indels 3; Gaps 2;
QY 56 GQFCFKPPGPKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKCRRLCDEGHGLEV 115
D 36 GLKLCQMCPEFTLVKDCDQHRKTAQCDFCPGVSPDPHTRPHCESCRHCNS--GLLV 93
QY 116 EINCRTQNTKCRCKPNEFCNSTVCEHCDP 145
D 94 R-NCITANAECACRNGMQCRDKECTECDP 122
RESULT 15
GQHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
A:Accession: A25218; A60204; S21689; I57638
R:Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725; PMID:3022937
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <JOH>
A:Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, S.; Grob,
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor.
A:Reference number: A60204; MUID:87085574; PMID:3025363
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31, 'T', '33-42, 'TT', '45-46, 'TX', '50-51, 'XX', '54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: this sequence has been corrected by a note added in proof to follow the nucleotide sequence of the complementary DNA.
R:Visavajjalala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H. Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor.
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M. Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor.
A:Reference number: I57638; MUID:89096903; PMID:2850481
A:Accession: I57638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on the extracellular domain may form part or all of a high-affinity receptor when it associates with the nerve growth factor.
C:Comment: This protein is thought to form a high-affinity receptor when it associates with the nerve growth factor.
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>

Search completed: May 9, 2003, 17:07:52
Job time : 31.8444 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:58:17 ; Search time 15.6873 Seconds
(without alignments)
885.720 Million cell updates/sec

Title: US-09-446-634A-22
Perfect score: 1804
Sequence: 1 MGIWTLPLVLTSLSS.....KDTSDSENSFRNEIQSLV 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	100.0	335	1 TNR6_HUMAN	P25445 homo sapien
2	1029.5	57.1	332	1 TNR6_PIG	O77736 sus scrofa
3	951	52.7	323	1 TNR6_BOVIN	P51867 bos taurus
4	856	47.5	327	1 TNR6_MOUSE	P25446 mus musculus
5	827.5	45.9	324	1 TNR6_RAT	O63199 rattus norv
6	211.5	11.7	381	1 T10B_MOUSE	O9qzm4 mus musculus
7	206	11.4	283	1 TR14_HUMAN	Q92956 homo sapien
8	199.5	11.1	417	1 TR12_HUMAN	Q93038 h tumor nec
9	197.5	10.9	468	1 T10A_HUMAN	O00220 homo sapien
10	197	10.9	440	1 T10B_HUMAN	O14763 homo sapien
11	189.5	10.5	176	1 TR23_MOUSE	O9er63 mus musculus
12	186	10.3	401	1 T11B_RAT	O08727 rattus norv
13	185.5	10.3	435	1 TNR3_HUMAN	P36941 homo sapien
14	183	10.1	401	1 T11B_HUMAN	O00300 homo sapien
15	182	10.1	401	1 T11B_MOUSE	O08712 mus musculus
16	182	10.1	416	1 TR16_CHICK	P18519 gallus gall
17	180	10.0	180	1 TR22_MOUSE	O9er62 mus musculus
18	177	9.8	455	1 TR1A_HUMAN	P19438 homo sapien
19	173.5	9.6	289	1 TNR5_MOUSE	P27512 mus musculus
20	169	9.4	386	1 T10D_HUMAN	Q9ubn6 homo sapien
21	164.5	9.1	250	1 TNR7_MOUSE	P41272 mus musculus
22	163.5	9.1	259	1 T10C_HUMAN	O14798 h tumor nec
23	161.5	9.0	277	1 TNR5_HUMAN	P25942 homo sapien
24	161	8.9	461	1 TR1A_PIG	P50555 sus scrofa
25	159.5	8.8	260	1 TNR7_HUMAN	P26842 homo sapien
26	159	8.8	427	1 TR16_HUMAN	P08138 homo sapien
27	156	8.6	425	1 TR16_RAT	P07174 rattus norv
28	153	8.5	349	1 CRMB_CAMPS	O8uya7 camelpox vi
29	151	8.4	417	1 TR16_MOUSE	O9z0w1 mus musculus
30	148.5	8.2	351	1 CRMB_CORPX	O73559 cowpox viru
31	147	8.1	415	1 TNR3_MOUSE	P50284 mus musculus
32	147	8.1	471	1 TR1A_BOVIN	O19131 bos taurus
33	146	8.1	454	1 TR1A_MOUSE	P25118 mus musculus

34	145	8.0	300	1 TR6B_HUMAN	O95407 homo sapien
35	144	8.0	272	1 TNR4_MOUSE	P47741 mus musculus
36	141.5	7.8	271	1 TNR4_RAT	P15725 rattus norv
37	141.3	7.8	461	1 TR1B_HUMAN	P20333 homo sapien
38	139	7.7	349	1 CRMB_VARV	P34015 variola vir
39	137.5	7.6	269	1 TNR5_BOVIN	Q28203 bos taurus
40	136.5	7.6	383	1 DLK_HUMAN	P80370 homo sapien
41	135	7.5	616	1 TR11_HUMAN	O9y6q6 homo sapien
42	134.5	7.5	625	1 TR11_MOUSE	O35305 mus musculus
43	129.5	7.2	326	1 VT2_MYXVL	P29825 myxoma viru
44	129.5	7.2	385	1 DLK_MOUSE	Q09163 mus musculus
45	124.5	6.9	325	1 VT2_SFVKA	P25943 Shope fibro

ALIGNMENTS

RESULT 1
TNR6_HUMAN
ID TNR6_HUMAN STANDARD; PRT; 335 AA.
AC P25445; Q14293; Q14294; Q14295; Q14292; Q16652;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91309137; PubMed=1713127;
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis.";
RL Cell 66:233-243(1991).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND
RP 321-335.
RX MEDLINE=92263122; PubMed=1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen.";
RL J. Biol. Chem. 267:10709-10715(1992).
[3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.
RX MEDLINE=95181785; PubMed=7533181;
RA Cascino I., Fiucci G., Papoff G., Ruberti G.;
RT "Three functional soluble forms of the human apoptosis-inducing Fas
RT molecule are produced by alternative splicing.";
RL J. Immunol. 154:2706-2713(1995).
[4]
RP SEQUENCE FROM N.A. (ISOFORM 5).
RX TISSUE-Peripheral blood lymphocytes;
RA Schaeuble C.E., Poehlmann R., Philippson P., Eibel H.;
RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
RX MEDLINE=96238926; PubMed=8648105;
RA Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;
RT "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants
RT prevents cell death in vitro.";
RL J. Immunol. 156:4622-4630(1996).
[6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE-Urinary bladder;

RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RX STRUCTURE BY NMR OF 218-335.
 RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
 RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
 RL Nature 384:638-641(1996).
 RN [8]
 RP VARIANT ALPS PRO-241.
 RX MEDLINE-95300225; PubMed-7540117;
 RA Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,
 RA Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;
 RT "Dominant interfering Fas gene mutations impair apoptosis in a human
 autoimmune lymphoproliferative syndrome.";
 RL Cell 81:935-946(1995).
 RN [9]
 RP VARIANT ALPS TYR-260.
 RX MEDLINE-97066823; PubMed-8929361;
 RA Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;
 RT "Fas gene mutations in the Canale-Smith syndrome, an inherited
 lymphoproliferative disorder associated with autoimmunity.";
 RL New Engl. J. Med. 335:1643-1649(1996).
 RN [10]
 RP VARIANTS ALPS TRP-121 AND CYS-232.
 RX MEDLINE-97180145; PubMed-9028321;
 RA Bettinardi A., Brugnani D., Quirios-Roldan E., Malagoli A.,
 RA La Grutta S., Corrao A., Notarangelo L.D.;
 RT "Missense mutations in the Fas gene resulting in autoimmune
 lymphoproliferative syndrome: a molecular and immunological
 analysis.";
 RL Blood 89:902-909(1997).
 RN [11]
 RP VARIANTS ALPS ASP-257 AND SER-310.
 RX MEDLINE-97180739; PubMed-9028957;
 RA Sneller M.C., Wang J., Dale J.K., Strober W., Middleton L.A., Choi Y.,
 RA Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
 RA Straus S.E.;
 RT "Clinical, immunologic, and genetic features of an autoimmune
 lymphoproliferative syndrome associated with abnormal lymphocyte
 apoptosis.";
 RL Blood 89:1341-1348(1997).
 RN [12]
 RP VARIANT ALPS ALA-28.
 RX MEDLINE-97463833; PubMed-9322534;
 RA Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,
 RA Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,
 RA Leviero M.;
 RT "Fas/Apo1 mutations and autoimmune lymphoproliferative syndrome in a
 patient with type 2 autoimmune hepatitis.";
 RL Gastroenterology 113:1384-1389(1997).
 RN [13]
 RP VARIANT ALPS VAL-260.
 RX MEDLINE-99038860; PubMed-9821419;
 RA Infante A.J., Britton H.A., DeNapoli T., Middleton L.A., Lenardo M.J.,
 RA Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;
 RT "The clinical spectrum in a large kindred with autoimmune
 lymphoproliferative syndrome caused by a Fas mutation that impairs
 lymphocyte apoptosis.";
 RL J. Pediatr. 133:629-633(1998).
 RN [14]
 RP VARIANTS ALPS LYS-241 AND GLN-250.
 RX MEDLINE-99192346; PubMed-10090885;
 RA Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,
 RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,
 RA Straus S.E., Puck J.M.;
 RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype
 influences penetrance.";
 RL Am. J. Hum. Genet. 64:1002-1014(1999).
 RN [15]
 RP VARIANT ALPS GLY-272.
 RX MEDLINE-99270228; PubMed-10340403;
 RA Peters A.M., Kohfink B., Martin H., Griesinger F., Worman B.,

RA Gahr M., Roesler J.;
 RL "Defective apoptosis due to a point mutation in the death domain of
 CD95 associated with autoimmune lymphoproliferative syndrome, T-cell
 lymphoma, and Hodgkin's disease.";
 RN Exp. Hematol. 27:868-874(1999).
 RP VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
 RX MEDLINE-99126461; PubMed-9927496;
 RA Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,
 RA Elkon K.B.;
 RT "The molecular basis for apoptotic defects in patients with CD95
 (Fas/Apo-1) mutations.";
 RL J. Clin. Invest. 103:355-363(1999).
 RN [17]
 RP VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;
 RX MEDLINE-99005325; PubMed-9787134;
 RA Groenbaek K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K.,
 RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;
 RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with
 extranodal disease and autoimmunity.";
 RL Blood 92:3018-3024(1998).
 RN [18]
 RP VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.
 RX MEDLINE-21311411; PubMed-11418480;
 RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
 RA Roosen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
 RA Fischer R.E., Jackson C.M., Lin A.Y., Baumler C., Siegert E.,
 RA Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;
 RT "The development of lymphomas in families with autoimmune
 lymphoproliferative syndrome with germline Fas mutations and
 defective lymphocyte apoptosis.";
 RL Blood 98:194-200(2001).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 recruits caspase-8 to the activated receptor. The resulting death-
 inducing signaling complex (DISC) performs caspase-8 proteolytic
 activation which initiates the subsequent cascade of caspases
 (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 mediated apoptosis may have a role in the induction of peripheral
 tolerance, in the antigen-stimulated suicide of mature T-cells, or
 both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC Secreted (isoforms 2 to 6).
 CC -1- ALTERNATIVE PRODUCTS: 6 isoforms; 1 (shown here), 2/Del2/d,
 CC 3/Del3/e, 4/b, 5/c and 6/TMDel/a; are produced by alternative
 CC splicing.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- DISEASE: Defects in TNFSF6 are a cause of autoimmune
 CC lymphoproliferative syndrome (ALPS), also known as Canale-Smith
 CC syndrome (CSS), a childhood syndrome involving hemolytic anemia
 CC and thrombocytopenia with massive lymphadenopathy and
 CC splenomegaly.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD95 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd95.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M67454; AAA63174.1; -;
 CC EMBL; X63717; CAA45250.1; -;
 CC EMBL; X89101; CAA61473.1; -;
 CC EMBL; Z47993; CAA88031.1; -;
 CC EMBL; Z47994; CAA88032.1; -;
 CC EMBL; Z47995; CAA88033.1; -;
 CC EMBL; Z70520; CAA94431.1; -;

DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.;"
RL DNA Cell Biol. 15:227-234(1996).
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR HMBL; U34794; AAC48546.1; --
DR HSPSP; P25445; IDDF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR Pfam: PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR.1; 2.
DR PROSITE; PS50050; TNFR_NGFR.2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
FT 17 323 SUPERFAMILY MEMBER 6.
FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 188 POTENTIAL.
FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
FT REPEAT 45 80 TNFR-CYS 1.
FT REPEAT 81 124 TNFR-CYS 2.
FT REPEAT 125 163 TNFR-CYS 3.
FT DOMAIN 238 306 DEATH.
FT DISULFID 45 56 BY SIMILARITY.
FT DISULFID 57 70 BY SIMILARITY.
FT DISULFID 60 79 BY SIMILARITY.
FT DISULFID 82 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 140 BY SIMILARITY.
FT DISULFID 143 154 BY SIMILARITY.
FT DISULFID 146 162 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 115 115 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;
Query Match 52.7%; Score 951; DB 1; Length 323;
Best Local Similarity 56.8%; Pred. No. 2.8e-64;
Matches 191; Conservative 47; Mismatches 84; Indels 14; Gaps 6;

QY 1 MLGIWTLPLVLTSVARLSKSVNAQVTDINSKGLERKTVTTVTQNLGLHHDGQFCH 60
Db 1 MSGIWWHLISLPIFISVSGPLSKGENAHMAGINSEGLKLN---ITEANSQCEGLYREHFQCC 57
QY 61 KPCPPGEKARDCTVNGDEPCQEGKEYTDKAHFSKRCRCRLCDHGHEVEINCT 120
Db 58 QPCPPGKRNKGDKRDGDTPECVLCSENGEYTDKSHHSDKRCISCDDEHGLEVEQNC 117
QY 121 RTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIEKCTLTSTNTKCKEGRSRLGW-LCL 179
Db 118 RTRNTKCRCKSNFFCNSTVCEHCDPCTKCEHGIIEKCTLTSTNTKCKEGRSHANSWALLI 177
QY 180 LLPLIPLVWKRVEQYTKRHKRKNESGSHESPLNPETVAINLSDVLSKYITTIAGV 239
Db 178 LLPLIPLVLIY---KVKRS-REKKNKDYCN-SASNDDEGRQLNLTVDLGRYIPSAEQ 231
QY 240 MTLQVQKGFVRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHOLHGHKEAYDTLIKDK 299
Db 232 MRITVEKFEVRKNGMEAEKIDIDHDNVHETAEQVQLLRNWHYSHGKKNAYCTLTSLP 291
QY 300 KANLCTLAETQTLIKDITSDSENSRNFIQSLV 335
Db 292 KA----LAETKIDIVMKDITNERENANLQENENLV 323

RESULT 4
ID TNFR6_MOUSE STANDARD; PRT; 327 AA.
AC P25446; Q9DCQ1;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92148151; PubMed=1371136;
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.;
RA Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
RT mouse Fas antigen.";
RL J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Koczan D., Ibrahim S.M., Thiesen H.J.;
RT "Role of a mutant fas receptor in a transgenic mouse.";
RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

the rat liver.";
Biochem. Biophys. Res. Commun. 198;666-674(1994).
-!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
-!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL; D26112; BAA03108.1; -
HSSP; P25445; 1DDF.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
Pfam; PF00531; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50030; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 21 BY SIMILARITY.
CHAIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). TNFR-CYS 1. TNFR-CYS 2. TNFR-CYS 3. DEATH. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). D25D583C909D09 CRC64; 324 AA; 36835 MW; 45.9%; Score 827.5; DB 1; Length 324; Best Local Similarity 49.0%; Pred. No. 4.9e-55; Matches 164; Conservative 55; Mismatches 103; Indels 13; Gaps 4;
Qy 1 MGIWTLPLVLTSLVARLSKSVNAQVDINSKGLERKTVTTVTQNLHHDGQFCH 60
Db 1 MLNIVAVLPVLG-----PELNVRMQGTDTSIFEGLELRKRSVRETDNNCSGLYQVGPCC 56
Qy 61 KCPGPKERKARDVNGDEPCVQCEKGVTDKRAHFSKRCRLCDGEGHLEVNCT 120
Db 57 QPCOPGERKVKDCTTSGAPCHCTGEGEYTDKRRKCAFCDEGHLEVNCT 116
Qy 121 RTQNTKCRKRPNFCNFTVCEHDCDPCKCE-HGIKECTLTSTNTKCEGSRSLGLWCL 179

Db 117 RTQNTKCRKRENYCNASLDCDHCYHCTSCGLEDELPCTRTSTNTKCKSSNYKLW--L 174
Qy 180 LLLPIPLIYVVRKKEVQKTCRKRRKNCQSHESPTLNPTVAINLSVDLSKYITTIAGV 239
Db 175 LLLPLGLAILEV-----FIYKRYKRPQDPESGIPSPESVPMNVSDVNLNKYIWTAEK 228
Qy 240 WTLQVKGKVRNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQLHGKKEAYDTLTKDLK 299
Db 229 MKICDAKFAHQHKIPESKIDIEHNSPDAAEQIKLLQCYWQSHGKGTGACQALQIGUR 288
Qy 300 KANLCTLAETKIITLTKDTSSENSFNREIQSL 334
Db 289 KANRCDIAETQAVWVEDHENSINSRNEGQSL 323
RESULT 6
T10B_MOUSE
ID T10B_MOUSE STANDARD; PRT; 381 AA.
AC Q9QZM4; Q9JUL5; Q9JUL6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (MK).
GN TNFRSF10B OR DR5 OR KILLER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE-99310501; PubMed-10383128;
RA Wu G.-S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) death receptor".
RT Cancer Res. 59:2770-2775(1999).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE-Spleen;
RC Nakamura Y., Tamari M., Watanabe O.;
RT "Mouse TRAIL receptor".
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.
CC -!- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC -!- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL; AF176833; AAD2656.1; -
DR EMBL; AB031081; BAA96462.1; -
DR EMBL; AB031082; BAA96463.1; -
DR HSSP; O14763; 1D0G.
DR MGD; MGI:1341090; Tnfrsf10b.

[illegible]

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
TISSUE=Lymphoid;
MEDLINE=97088617; PubMed=8934525;
Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
Grinham C.J., Brown R., Farrow S.N.;
"A death-domain-containing receptor that mediates apoptosis.";
Nature 384:372-375(1996).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Umbilical vein endothelial cells;
MEDLINE=97081063; PubMed=8875942;
Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
"Signal transduction by DR3, a death domain-containing receptor
related to TNFR-1 and CD95.";
Science 274:990-992(1996).
[3]
SEQUENCE FROM N.A.
Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Heart;
MEDLINE=971148200; PubMed=8994832;
Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
Goddard A.D., Bauer K.D., Ashkenazi A.;
"Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kappa-B.";
Curr. Biol. 6:1669-1676(1996).
[5]
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
MEDLINE=9727273; PubMed=9114039;
Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
McMichael A.J., Bell J.I.;
"LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
[6]
SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
MEDLINE=98113360; PubMed=9446802;
Warzocha K., Ribeiro P., Charlot C., Renard N., Colffier B.,
Salles G.;
"A new death receptor 3 isoform: expression in human lymphoid cell
lines and non-Hodgkin's lymphomas.";
Biochem. Biophys. Res. Commun. 242:376-379(1998).
[7]
SEQUENCE FROM N.A. (ISOFORM 1).
Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 4-417 FROM N.A.
TISSUE=Brain, and Fetal lung;
MEDLINE=97205335; PubMed=9052839;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Browning J.L., MacDonald H.R., Tschoopp J.;
"TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
Immunity 6:79-88(1997).
[9]
SEQUENCE OF 7-417 FROM N.A.
TISSUE=Brain;
Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly
with the adaptor TRADD. Mediates activation of NF-kappaB and
induces apoptosis. May play a role in regulating lymphocyte
homeostasis.
-1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO

RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
RL EMBO J. 16:5386-5397(1997).
RN [2]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE
RZ SPLICING.
RX MEDLINE-97431692; PubMed-9285725;
RA Srean G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,
RA McMichael A.J., Bell J.I.;
RT "TRICK2, a new alternatively spliced receptor that transduces the
RT cytotoxic signal from TRAIL";
RL Curr. Biol. 7:693-696(1997).
RN [3]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RZ TISSUE=Liver, and Spleen;
RX MEDLINE-98039016; PubMed-9373179;
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,
RA Tschoep J.;
RT "Characterization of two receptors for TRAIL";
RL FEBS Lett. 416:329-334(1997).
RN [4]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ TISSUE=Ovary;
RX MEDLINE-97467719; PubMed-9326928;
RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,
RA Krantz J.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,
RA Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;
RT "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor
RT gene";
RL Nat. Genet. 17:141-143(1997).
RN [5]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ MEDLINE-97390508; PubMed-9242610;
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL";
RL Science 277:815-818(1997).
RN [6]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ MEDLINE-97467318; PubMed-9325248;
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.;
RT "Identification and molecular cloning of two novel receptors for the
RT cytotoxic ligand TRAIL";
RL J. Biol. Chem. 272:25417-25420(1997).
RN [7]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ MEDLINE-98090092; PubMed-9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
RT FADD-dependent apoptosis and activate the NF-kappaB pathway";
RL Immunity 7:821-830(1997).
RN [8]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ MEDLINE-97390509; PubMed-9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors";
RL Science 277:818-821(1997).
RN [9]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RZ Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2
RT gene in colorectal carcinoma";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ Cao X., Zhang W., Wan T.;
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RZ Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;

RT "Homo sapiens homolog of tumor necrosis factor receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RZ TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
RZ MEDLINE-20017054; PubMed-10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Frigering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5";
RL Mol. Cell 4:563-571(1999).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
RZ PubMed-10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Srean G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation";
RL Nat. Struct. Biol. 6:1048-1053(1999).
CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
CC adaptor molecule FADD recruits caspase-8 to the activated
CC receptor. The resulting death-inducing signaling complex (DISC)
CC performs caspase-8 proteolytic activation which initiates the
CC subsequent cascade of caspases (aspartate-specific cysteine
CC proteases) mediating apoptosis. Promotes the activation of NF-
CC kappaB.
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/TRICK2B (SHOWN HERE)
CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;
CC very highly expressed in tumor cell lines such as HeLa S3, K562,
CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral
CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,
CC ovary, uterus, placenta, testis, esophagus, stomach and throughout
CC the intestinal tract; not detectable in brain.
CC -1- INDUCTION: TNFSF10B is regulated by the tumor suppressor p53.
CC -1- DISEASE: Defects in TNFSF10B may be a cause of squamous cell
CC carcinoma of the head and neck.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; AF016849; AAC51778.1; -
DR EMBL; AF018657; AAB70577.1; -
DR EMBL; AF018658; AAB70578.1; -
DR EMBL; AF016266; AAB81180.1; -
DR EMBL; AF022386; AAB71949.1; -
DR EMBL; AF012628; AAB67109.1; -
DR EMBL; AF020501; AAB71412.1; -
DR EMBL; AF016268; AAC01565.1; -
DR EMBL; AF012535; AAB67103.1; -
DR EMBL; AB014718; BAA33723.1; -
DR EMBL; AB014710; BAA33723.1; JOINED.
DR EMBL; AB014712; BAA33723.1; JOINED.
DR EMBL; AB014713; BAA33723.1; JOINED.
DR EMBL; AB014714; BAA33723.1; JOINED.
DR EMBL; AB014715; BAA33723.1; JOINED.
DR EMBL; AB014716; BAA33723.1; JOINED.
DR EMBL; AB014717; BAA33723.1; JOINED.
DR EMBL; AF153687; AAF75587.1; -

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DR EMBL; AF192548; AAF07175.1; -
DR EMBL; BC001281; AAH01281.1; -
DR Genew; HGNC:11905; TNFRSF10B.
DR MIM; 603612; -
DR PDB; 1D0G; 22-OCT-99.
DR PDB; 1D4V; 01-NOV-99.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR Pfam; PF00531; Death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Transmembrane; Repeat; Signal;
KW Alternative splicing; 3D-structure.
FT SIGNAL 1 55
FT CHAIN 56 440
      TUMOR NECROSIS FACTOR RECEPTOR
      SUPERFAMILY MEMBER 10B.
      EXTRACELLULAR (POTENTIAL).
      POTENTIAL.
      CYTOPLASMIC (POTENTIAL).
      TNFR-CYS 1.
      TNFR-CYS 2.
      TNFR-CYS 3.
      TAPE.
      DEATH.
      POLY-GLY.
      DOMAIN 56 210
      TRANSMEM 211 231
      DOMAIN 232 440
      REPEAT 57 94
      REPEAT 97 137
      REPEAT 138 178
      REPEAT 192 206
      REPEAT 339 422
      DOMAIN 423 440
      DISULFID 81 94
      DISULFID 97 113
      DISULFID 116 129
      DISULFID 119 137
      Query Match
      Best Local Similarity 10.9%; Score 197; DB 1; Length 440;
      Matches 77; Conservative 34; Mismatches 93; Indels 86; Gaps 14;
      QY 8 LPLVLTSLVARLSKSNVAQVTDINSKGL--ELRKTVTVTQNLGLHDPGQCHRPCKPP 65
      DB 38 LVLVAVALL-----VSAESALITQDAPQRAAPQKRSPSEGL-----CPP 83
      QY 66 GERKARDCTVNGDEPCVPCQEGKEYTDKAHSSKRCRCRLCDGHLGVEIN-CTRQTN 124
      DB 84 GH-----ISEGRCISCKYQDYSTHWNDLLFLCLTRCDG---EVELSPCTTRN 134
      QY 125 TKCRKPNCFTVCEHCDPC-TKEHGIK--ECTLTSTNKC--KEGSRSLNGLWCL 179
      DB 135 TVQCCEGTFRDEDSPEMCRKRTGCPGMVKVGDCTPWSIDIECVHESGT----- 185
      QY 180 LLLPIPLIWMKRKEVQKCRKRKENOGSHESPTINPTVAINLSDVLSKYI---TTIA 237
      DB 186 -----KHSGEAPAVEETVTSSTGTPA---SPCSLSGLIIGTVTA 221
      QY 238 GVM-----TLSQVKGVRKNGVNEAKIDEIK-----NDNV 267
      DB 222 AVVLIIVAVFCKSLWKVLPYLKIGCSGGGDPERVDRSSRPGADNV 271
      RESULT 11
      TR23_MOUSE
      ID TR23_MOUSE STANDARD; PRT; 176 AA.
      AC Q9ER63; Q8VHCO;
      DT 15-JUN-2002 (Rel. 41, Created)
      DT 15-JUN-2002 (Rel. 41, Last sequence update)
      DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
      factor receptor p60 homolog 1) (TNF receptor family member SOB).
      GN TNFRSF23 OR TNFRSF1A1 OR TNFRH1.
      OS Mus musculus (Mouse).
      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RL Implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
[2]
RN RP SEQUENCE FROM N.A.
RA Pan G., Mao W., Rissler P.;
RT "Characterization of SOB, a member of the TNFR family.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
      -----
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      or send an email to license@isb-sib.ch).
      -----
      EMBL; AJ278264; CAC16405.1; -
      EMBL; AJ278505; CAC27352.1; -
      EMBL; AY046550; AAL05072.1; -
      HSSP; P19438; 1EXT.
      DR MGD; MGI:1930269; Tnfrsf23.
      DR InterPro; IPR001368; TNFR_c6.
      DR Pfam; PF00020; TNFR_c6; 3.
      DR SMART; SM00208; TNFR; 3.
      DR PROSITE; PS00500; TNFR_NGFR_2; 2.
      KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
      FT DOMAIN 1 9
      FT TRANSMEM 10 30
      FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
      FT (POTENTIAL).
      FT DOMAIN 31 176
      FT REPEAT 31 72
      FT REPEAT 74 114
      FT REPEAT 115 155
      FT DISULFID 38 49
      FT DISULFID 50 63
      FT DISULFID 53 72
      FT DISULFID 75 90
      FT DISULFID 93 106
      FT DISULFID 96 114
      FT DISULFID 116 131
      FT DISULFID 134 147
      FT DISULFID 137 155
      FT CARBOHYD 148 148
      FT N-LINKED (GLCNAC...) (POTENTIAL).
      SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DDB7D CRC64;
      Query Match
      Best Local Similarity 10.5%; Score 189.5; DB 1; Length 176;
      Matches 42; Conservative 19; Mismatches 68; Indels 7; Gaps 5;
      QY 50 EGLHHDGQFCHRPCKPPGERKARDCTVNGDEPCVPCQEGKEYTDKAHSSKRCRCRLCDE 109
      DB 40 DGEYQSDNVCCCKTSPGTFVKAAPKIPHTQGGCKCHPG-TFTGKNGLHDCELSTCDK 98
      QY 110 GHGLEVEINCRFTQNTKCRKRN-PFCNSTVCEHCDPCTKEHGI--INCKTLTNTKCK 166
      DB 99 DONMYAD--CSATDRKCECQIGLYYDPKFPESCRPCTKCPQGPVPLQECNSTANTVCS 156
      QY 167 BEGSRSLNGLWCLLL 182
      DB 157 SSVSNPR-NWLFLLML 171
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RESULT 12
T11B.RAT
ID T11B.RAT STANDARD; PRT; 401 AA.
AC O08727:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 11b precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Sugis S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Upregulated by osteopontin.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC -----
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CC -----
DR EMBL: U94330; AAB33707.1;
DR HSP; P25942; ICDF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT SITE 41 54
FT DISULFID 41 54
FT DISULFID 64 80
FT DISULFID 65 80
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FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT SEQUENCE 401 AA; 46192 MW; FECA31FD4E573A CRC64;
Query Match 10.3%; Score 186; DB 1; Length 401;
Best Local Similarity 25.8%; Pred. No. 6.6e-07;
Matches 77; Conservative 36; Mismatches 110; Indels 76; Gaps 16;
QY 42 TTVETQNLGLHHDGQ-----FCHKPCPPGKERKARDCTVNGDEPCVPCQSGKEVTKAH 96
DB 19 TTOETFPKYLHYDPETGROLLCDK-CAPGYLKHQCTVR-RKTLGVPCPD-YSTDSWH 75
QY 97 FSSKRCRCR-LCDGSHGLEVEINCTRTONTKCRCKPNFFCNSTVC---EHGDP----- 145
DB 76 TSDECVYCSVCKELQVQKB--CNRTHNRVCEEGEGRYLELEFCLKHRSPPGLGVLOA 133
QY 146 -----CTKCEHGIIKECTLTSTNCKEBSRNSLGLCLLLPIPLIYVVRKKEYQK 197
DB 134 GTPERNTVCKRCPDGFSGET-SSKAPCRKHTNCSSLG---LLL-----IQK 176
QY 198 -----TCRKHRENQSGSHESPTLNPE-----TVAINLSDVLSKYITTTAGVMTLSQV 245
DB 177 GNATHDNCVSGNREATQCGIDVTLCIEAFPRFAPVTKIIPNWLVLVDLSLPGTK----- 231
QY 246 KGFVRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNHOLHGCKEAYDTFLIKLKKANLC 304
DB 232 -----VNAESVERIKRRH--SSQEQTFOLLKLMKHQNDQEMVKKIQDI---DLC 277
RESULT 13
TNR3_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE protein) (Tumor necrosis factor C receptor).
GN LYBR OR TNFRSF3 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RA "Construction and evaluation of a hncDNA library of human 12p
RA transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RA MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RA "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
RN [4]
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RP CHARACTERIZATION.
RX MEDLINE-99223511; PubMed-10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RL death in Hela cells.";
RN J. Biol. Chem. 274:11868-11873(1999).
RP FUNCTION
RX MEDLINE-20261554; PubMed-10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RT Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RL "The lymphotoxin-beta receptor is necessary and sufficient for
RN LIGHT-mediated apoptosis of tumor cells.";
CC J. Biol. Chem. 275:14307-14315(2000).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -!- SUBUNIT: Self-associates.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC
CC EMBL: L04270; AAA36757.1;
CC EMBL: BC026262; AAH26262.1;
CC HSSP: P25942; 1CDF.
CC Genes: HGNC:6718; LTBR.
CC MIM: 600979;
CC InterPro: IPR001368; TNFR_C6.
CC Pfam: PF00020; TNFR_C6; 4.
CC ProDom: PD000771; TNFR_C6; 1.
CC SMART: SM00208; TNFR; 4.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00050; TNFR_NGFR_2; 3.
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
CC SIGNAL 1 30 POTENTIAL
CC CHAIN 31 435
CC
CC DOMAIN 31 227
CC TRANSMEM 228 248
CC DOMAIN 249 435
CC REPEAT 42 81
CC REPEAT 82 124
CC REPEAT 125 168
CC REPEAT 169 211
CC DISULFID 43 58
CC DISULFID 59 72
CC DISULFID 62 80
CC DISULFID 83 98
CC DISULFID 101 116
CC DISULFID 104 124
CC DISULFID 126 132
CC DISULFID 139 148
CC DISULFID 142 167
CC DISULFID 170 185
CC CARBOHYD 40 40
CC CARBOHYD 177 177
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 435 AA; 46709 MW; 624626E022F656F CRC64;
CC
CC Query Match 10.3%; Score 185.5; DB 1; Length 435;
CC Best Local Similarity 25.3%; Pred. No. 7.9e-07;
CC Matches 63; Conservative 25; Mismatches 82; Indels 79; Gaps 12;
CC
CC 43 TVEITNQLGHDGFCFKPCPPGKRCARDCTVNGEDPCVPCQEGKEYTDKAHFSSKCR 102
CC 42 TCRDQKEYEYEPQHRICSCRCPPGTYVSARKSRIDTV-CATCAE-NSYNEHWNYLTICQ 99

QY 103 RCRLCDGHEGLVEINCTRTQNTKCRCKPNFFC-----NSTVCE----- 141
DB 100 LCRPCDPVMGLEETAPCTSKRKTCRCOPCFCAAWALECTHCELLSDCPCPGTEAEALKDE 159
QY 142 -----HCDCP-----TKCEH-GLIKEC---TLTSNTKCK---EGSR 171
DB 160 VGKGNHCVCKAGHFQNTSSPSARCOPHTRCENOGIVEAPCTAGSDTTCCKNPLEPLPP 219
QY 172 SNLGLWLCLLLLPL-----IVVVKREVKQTCR-----KHKRKN-----G 208
DB 220 EWSGTMLMLAVLPLAFFLLLATVFCIW---KSHPSLCRKLKGLSKRRPQGBGNPVAG 276
QY 209 SHESPTLNP 217
DB 277 SWEPKKAHP 285

RESULT 14
ID T11B_HUMAN STANDARD; PRT; 401 AA.
AC O00300; O60236; Q9UHP4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (osteoprotegerin) (osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPB OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE-97262071; PubMed-9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luthy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Darvay E., Bucay N., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Campbell P., Sander S., Van G., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Suggs S., Boyle W.J., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE-98151033; PubMed-9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RL osteoclastogenesis in vitro.";
RN Endocrinology 139:1329-1337(1998).
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE-98351569; PubMed-9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE-98238645; PubMed-9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;

T11B_MOUSE
 ID T11B_MOUSE STANDARD; PRT; 401 AA.
 AC O08712; 070202;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis Inhibitory factor).
 GN TNFRSF11B OR OPG OR OCIF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Kidney;
 RA MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RA of bone density.";
 RT Cell 89:309-319(1997).
 RL [2]
 RN SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
 RP AND ARG-296.
 RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
 RA MEDLINE=98382527; PubMed=9714833;
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
 RA Higashio K.;
 RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
 RA gene and its expression in embryogenesis.";
 RT Gene 215:339-343(1998).
 RL [3]
 RN FUNCTION.
 RP MEDLINE=21060987; PubMed=10952716;
 RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
 RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
 RA Simonet W.S.;
 RA "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
 RA osteoclasts and prevents vascular calcification by blocking a process
 RA resembling osteoclastogenesis.";
 RT J. Exp. Med. 192:463-474(2000).
 RL [4]
 RN FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 RP its function in osteoclastogenesis. Inhibits the activation of
 RC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC [5]
 RN SUBUNIT: Homodimer.
 RP [6]
 RN SUBCELLULAR LOCATION: Secreted.
 RP [7]
 RN TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
 RP intestines and calvaria. Highly expressed in decidua and placenta,
 CC and in embryo.
 CC [8]
 RN DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
 RP whereas expression decreases at day 11 and increases from day 15
 CC to 17. On day 15 found in developing bone primordia,
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,
 CC abdominal aorta and midgut.
 CC [9]
 RN INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
 RP 1,25-dihydroxyvitamin D3 and parathyroid hormone.
 CC [10]
 RN SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 RP [11]
 RN SIMILARITY: CONTAINS 2 DEATH DOMAINS.
 CC [12]
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 DR EMBL; U94331; AAB53708.1; -;
 DR EMBL; AB013898; BAA28269.1; -;
 DR EMBL; AB013903; BAA33388.1; -;
 DR EMBL; AB013899; BAA33388.1; JOINED.
 DR EMBL; AB013900; BAA33388.1; JOINED.
 DR EMBL; AB013901; BAA33388.1; JOINED.
 DR EMBL; AB013902; BAA33388.1; JOINED.
 DR HSSP; P25942; ICDP.
 DR MGD; MGI:109587; Tnf1b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR ProDom; PD000771; TNFR_C6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00017; DEATH DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT FT BY SIMILARITY.
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 11B.
 FT REPEAT 24 62
 FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT DOMAIN 198 269
 FT DOMAIN 283 365
 FT SITE 400 400
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 107 118
 FT DISULFID 124 142
 FT DISULFID 145 160
 FT DISULFID 166 185
 FT CARBOHYD 98 98
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 138 138
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
 SQ
 Query Match 10.1%; Score 182; DB 1; Length 401;
 Best Local Similarity 25.5%; Pred. No. 1.3e-06;
 Matches 76; Conservative 34; Mismatches 114; Indels 74; Gaps 15;
 QY 42 TTVTQNLGLHHDGQFCHK----PCPCERKARCTVNGDEPDCVPCQEGKEYTDKAHF 97
 DB 19 TQETPLPKYLYHDETGHQLLCKDCAPCTYLKQCTVR-RKTLCPVCPD-HSYTDSWHT 76
 QY 98 SSKRCRR-LCDEGHGHEVEINCTQNTKCRKFNFCNVTVC---EHCDDP-----145
 DB 77 SDECVCYSPVKELQSVQKE--CNTHNRVCECEGRYLEFCLKHRCPPGSGVQAG 134
 QY 146 -----CTKEHGIIKECTITNTKCKEGRSRNLGWLCLLLPIPLVWKRKEVQK- 197
 DB 135 TPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFG----LLL-----IQKG 177

[illegible]

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